

P

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

## STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>5</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>7/23/01</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>7/24/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>02</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 17:06:07 ; Search time 69.82 Seconds  
(Without alignments)  
41.689 Million cell updates/sec

Title: US-09-351-296-16

Perfect score: 22  
Sequence: 1 TATKQAEAAAPVYESKWRMLEA 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 425026 segs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5654

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

SPPREMBL\_16:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.unclassified:\*  
13: sp.vertebrate:\*  
14: sp.virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4	18.2	7	2	047477	047477 escherichia
2	4	18.2	11	2	09K332	09K332 staphylococ
3	4	18.2	11	4	014759	014759 homo sapien
4	4	18.2	11	4	09UCR1	09UCR1 homo sapien
5	4	18.2	13	14	069394	069394 pseudorabie
6	4	18.2	15	6	09T009	09T009 bos taurus
7	4	18.2	15	6	09TR40	09TR40 bos taurus
8	4	18.2	15	8	09T210	09T210 nicotiana t
9	4	18.2	15	11	09Q0Z5	09Q0Z5 mus sp. 38-
10	4	18.2	16	2	09KHM6	09KHM6 synechococ
11	4	18.2	16	10	09S8L1	09S8L1 sorghum bic
12	4	18.2	16	11	09QZV3	09QZV3 mus musculu
13	4	18.2	16	11	09Q0Y8	09Q0Y8 cricetus
14	4	18.2	17	11	061932	061932 mus musculu
15	4	18.2	19	10	P81895	P81895 solanum tub
16	4	18.2	19	14	069396	069396 pseudorabie
17	4	18.2	20	2	069176	069176 chlamydia t
18	4	18.2	20	2	053520	053520 chlamydia t
19	4	18.2	20	2	085509	085509 chlamydia t

20	4	18.2	20	2	085510	085510 chlamydia t
21	4	18.2	20	2	085512	085512 chlamydia t
22	4	18.2	20	2	085514	085514 chlamydia t
23	4	18.2	20	2	085517	085517 chlamydia t
24	4	18.2	20	2	085519	085519 chlamydia t
25	4	18.2	20	2	085520	085520 chlamydia t
26	4	18.2	20	2	085521	085521 chlamydia t
27	4	18.2	20	2	085522	085522 chlamydia t
28	4	18.2	20	2	085523	085523 chlamydia t
29	4	18.2	20	2	085525	085525 chlamydia t
30	4	18.2	20	2	085526	085526 chlamydia t
31	4	18.2	20	2	085528	085528 chlamydia t
32	4	18.2	20	2	085530	085530 chlamydia t
33	4	18.2	20	2	085531	085531 chlamydia t
34	4	18.2	20	2	085533	085533 chlamydia t
35	4	18.2	20	4	09Q0H2	09Q0H2 homo sapien
36	4	18.2	20	8	033294	033294 zeo mays (m
37	4	18.2	20	9	037944	037944 lactococcus
38	4	18.2	21	8	092YX6	092YX6 orussus ter
39	4	18.2	22	2	P81150	P81150 desulfovibr
40	4	18.2	22	2	09R403	09R403 pseudomonas
41	4	18.2	22	5	09TW08	09TW08 crithidia t
42	4	18.2	22	8	09T2H8	09T2H8 nicotiana t
43	4	18.2	22	13	09PS65	09PS65 oncorhynch
44	4	18.2	22	14	087084	087084 pseudorabie
45	4	18.2	22	14	087085	087085 pseudorabie

## ALIGNMENTS

RESULT 1  
ID 047477 PRELIMINARY; PRT; 7 AA.  
AC 047477;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
DE TPI PROTEIN (FRAGMENT).  
GN TPI.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE OF 7-7 FROM N.A.  
RX MEDLINE=85203917; PubMed=3158524;  
RA Hellinga H.W.; Evans P.R.;  
RT "Nucleotide sequence and high-level expression of the major  
RT Escherichia coli phosphofructokinase";  
RL Eur. J. Biochem. 149:363-373(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Evans P.;  
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X02519; CAA26359.1; -.  
FT NON\_TER  
SQ SEQUENCE 7 AA: 773 MW; 7416D33DDDB1DB0 CRC64;

Query Match 18.2%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAA 9  
Db 1 AEAA 4  
RESULT 2  
ID 09K332 PRELIMINARY; PRT; 11 AA.  
AC 09K332;

DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE GEN (FRAGMENT).  
CN Staphylococcus aureus.  
OS Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-VARIOUS STRAINS;  
RX MEDLINE=20187516; PubMed=10722640;  
RA Cramton S.E., Schnell N.F., Gotz F., Bruckner R.;  
RT "Identification of a new repetitive element in Staphylococcus  
RT aureus";  
RL Infect. Immun. 68:2344-2348(2000).  
DR EMBL; AF195967; AAF60251.1; -;  
DR EMBL; AF195963; AAF60243.1; -;  
DR EMBL; AF195964; AAF60245.1; -;  
DR EMBL; AF195965; AAF60247.1; -;  
DR EMBL; AF195966; AAF60249.1; -;  
DR InterPro; IPR001189; -;  
DR ProDom; PD000475; -; 1.  
FT NON\_TER 1  
SQ SEQUENCE 11 AA; 1262 MW; 4F978F86A8A1A723 CRC64;

Query Match 18.2%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TKQA 6  
Db 8 TKQA 11

RESULT 3  
ID 014759 PRELIMINARY; PRT; 11 AA.  
AC 014759;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
DE LYMPHOCYTE CYTOSOLIC PROTEIN 2 (FRAGMENT).  
GN LCP2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stenden S.L.F., Carr L.L., Clements J.L., Molto D.G., Koretzky G.A.;  
RL Genomics 0:0-0(0).  
DR EMBL; U44065; AAA93308.1; -;  
FT NON\_TER 1  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1242 MW; D695104224072DD CRC64;

Query Match 18.2%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAA 9  
Db 2 AEAA 5

RESULT 4  
ID 09UCR1 PRELIMINARY; PRT; 11 AA.  
AC 09UCR1;

DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE AUTOTAXIN.  
CN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=92129337; PubMed=1733949;  
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cloce V.,  
RA Schiffrmann E., Liotta L.A.;  
RT "Identification, purification, and partial sequence analysis of  
RT autotaxin, a novel motility-stimulating protein.";  
RL J. Biol. Chem. 267:2524-2529(1992).  
SQ SEQUENCE 11 AA; 1171 MW; 273615AA0437737 CRC64;

Query Match 18.2%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATK 4  
Db 8 TATK 11

RESULT 5  
ID 069394 PRELIMINARY; PRT; 13 AA.  
AC 069394;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE GLYCOPROTEIN PRECURSOR (FRAGMENT).  
OS Pseudorabies virus.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
OX NCBI\_TaxID=10345;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93227568; PubMed=8385840;  
RA Ryan P., Robbins A., Whealy M., Enquist L.W.;  
RT "Overall signal sequence hydrophobicity determines the in vivo  
RT translocation efficiency of a herpesvirus glycoprotein.";  
RL Virus Genes 7:5-21(1993).  
DR EMBL; M77773; AAA73134.1; -;  
KW Signal.  
FT SIGNAL 1  
FT CHAIN 12  
FT NON\_TER 13  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1274 MW; 7D36E7528A6F9DC4 CRC64;

Query Match 18.2%; Score 4; DB 14; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAP 11  
Db 10 AAAP 13

RESULT 6  
ID 09TOO9 PRELIMINARY; PRT; 15 AA.  
AC 09TOO9;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
DE GLUTAMATE DEHYDROGENASE ISOFORM I (EC 1.4.1.2) (FRAGMENT).  
OS Bos taurus (Bovine).



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96061967; PubMed=7588764;  
 RA Cho S.W., Lee J., Choi S.Y.;  
 RT "Two soluble forms of glutamate dehydrogenase isoproteins from bovine brain";  
 RL Eur. J. Biochem. 233:340-346(1995).  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE=96043916; PubMed=7581004;  
 RA Lee J., Kim S.W., Cho S.W.;  
 RT "A novel glutamate dehydrogenase from bovine brain: purification and characterization";  
 RL Biochem. Mol. Biol. Int. 36:1087-1096(1995).  
 SQ SEQUENCE 15 AA; 1754 MW; 65F7CD91023AEBA CRC64;

Query Match 18.2%; Score 4; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAAA 10  
 Db 2 EAAA 5

RESULT 7  
 O9TR40 PRELIMINARY; PRT; 15 AA.  
 AC O9TR40;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE GLUTAMATE DEHYDROGENASE ISOFORM II (EC 1.4.1.2) (FRAGMENT).  
 OS Bos taurus (Bovinae).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96061967; PubMed=7588764;  
 RA Cho S.W., Lee J., Choi S.Y.;  
 RT "Two soluble forms of glutamate dehydrogenase isoproteins from bovine brain";  
 RL Eur. J. Biochem. 233:340-346(1995).  
 SQ SEQUENCE 15 AA; 1724 MW; 65F7CD91023AEBA CRC64;

Query Match 18.2%; Score 4; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAAA 10  
 Db 2 EAAA 5

RESULT 8  
 O9T210 PRELIMINARY; PRT; 15 AA.  
 AC O9T210;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE 18.5 KDA PHOTOSYSTEM I PSAD PROTEIN (FRAGMENT).  
 OS Nicotiana tomentosiformis (Tobacco).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
 OC Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4098;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94105345; PubMed=8278548;  
 RA Obokata J., Mikami K., Hayashida N., Nakamura M., Sugiyama M.;  
 RT "Molecular heterogeneity of photosystem I. psad, psae, psaf, psah, and psal are all present in isoforms in Nicotiana spp.";  
 RL Plant Physiol. 102:1259-1267(1993).  
 SQ SEQUENCE 15 AA; 1429 MW; D2388E48B5760A8 CRC64;

Query Match 18.2%; Score 4; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAAA 10  
 Db 3 EAAA 6

RESULT 9  
 O9QUZ5 PRELIMINARY; PRT; 15 AA.  
 AC O9QUZ5;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE 38-42 KDA COSTIMULATORY FACTOR (FRAGMENT).  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96007483; PubMed=7559503;  
 RA Vinay D.S., Raju M., Verma R.K., Mishra G.C.;  
 RT "Characterization of novel costimulatory molecules. A protein of 38-42 kDa from B cell surface is concerned with T cell activation and differentiation";  
 RL J. Biol. Chem. 270:23429-23436(1995).  
 SQ SEQUENCE 15 AA; 1758 MW; F10C664C976A5D19 CRC64;

Query Match 18.2%; Score 4; DB 11; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEAA 9  
 Db 2 AEAA 5

RESULT 10  
 O9KHM6 PRELIMINARY; PRT; 16 AA.  
 AC O9KHM6;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE PROTEOLYSIS TAG (FRAGMENT).  
 OS Synechococcus sp. PCC 6307.  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
 OX NCBI\_TaxID=59930;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20345063; PubMed=10884408;  
 RA Keller K.C., Shapiro L., Williams K.P.;  
 RT "tmRNAs that encode proteolysis-inducing tags are found in all known bacterial genomes: A two-piece tmRNA functions in Caulobacter";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:7778-7783(2000).  
 DR EMBL; AF251551; AF87980.1; -.

FT NON\_TER 1  
SQ SEQUENCE 16 AA; 1685 MW; 76245B0FB9AC6C62 CRC64;

Query Match 18.2%; Score 4; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPV 12  
Db 11 AAPV 14

RESULT 11

O9S8L1 PRELIMINARY; PRT; 16 AA.

AC O9S8L1;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE CYNOCROME P-450 (FRAGMENT).  
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;  
OC Andropogoneae; Sorghum.  
OX NCBI\_TaxID=4558;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95024036; Pubmed=7937883;  
RA Slibesen O., Koch B., Halkier B.A., Moller B.L.;  
RT "Isolation of the heme-thiolate enzyme cytochrome P-450<sup>TYR</sup>, which  
RT catalyzes the committed step in the biosynthesis of the cyanogenic  
RT glucoside dhurrin in Sorghum bicolor (L.) Moench.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:9740-9744(1994).  
SQ SEQUENCE 16 AA; 1516 MW; D548BD84E99FD489 CRC64;

Query Match 18.2%; Score 4; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAAA 10  
Db 6 EAAA 9

RESULT 12

O9QZT3 PRELIMINARY; PRT; 16 AA.

AC O9QZT3;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE R29144/1 (FRAGMENT).  
GN R29144/1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129;  
RX MEDLINE=99330555; Pubmed=10400995;  
RA Smith D.P., Spicer J., Smith A., Swift S., Ashworth A.;  
RT "The mouse peltz-jeghers syndrome gene lkb1 encodes a nuclear protein  
RT kinase.";  
RL Hum. Mol. Genet. 8:1479-1485(1999).  
DR EMBL; AF145697; AAD5370.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 16 AA; 1518 MW; D6C720E4BFF0A1D2 CRC64;

Query Match 18.2%; Score 4; DB 11; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AAP 11  
Db 5 AAP 8

RESULT 13

O9QUT8 PRELIMINARY; PRT; 16 AA.

AC O9QUT8;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE HISTONE H1 (FRAGMENT).  
OS Cricetus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetus.  
OX NCBI\_TaxID=10029;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96070893; Pubmed=7499230;  
RA Gurley L.R., Valdez J.G., Buchanan J.S.;  
RT "Characterization of the mitotic specific phosphorylation site of  
RT histone H1. Absence of a consensus sequence for the p34cdc2/cyclin B  
RT kinase.";  
RL J. Biol. Chem. 270:27653-27660(1995).  
SQ SEQUENCE 16 AA; 1479 MW; 75EB48873728BC8A CRC64;

Query Match 18.2%; Score 4; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AAP 11  
Db 9 AAP 12

RESULT 14

O61932 PRELIMINARY; PRT; 17 AA.

AC O61932;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT FAST (ADULT SKELETAL MUSCLE  
DE MYOSIN HEAVY CHAIN) (FRAGMENT).  
GN MYH4 OR MYHSE.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84061805; Pubmed=6196357;  
RA Weyder A., Dabdas P., Caravatt M., Minty A., Bugalsky G., Cohen A.,  
RA Robert B., Buckingham M.E.;  
RT "Sequential accumulation of mRNAs encoding different myosin heavy  
RT chain isoforms during skeletal muscle development in vivo detected  
RT with a recombinant plasmid identified as coding for an adult fast  
RT myosin heavy chain from mouse skeletal muscle.";  
RL J. Biol. Chem. 258:13867-13874(1983).  
DR EMBL; K00986; AAA39792.1; -.  
KW MGD; MGI:1339713; myh4.  
MYOSIN.  
FT NON\_TER 1  
SQ SEQUENCE 17 AA; 1985 MW; 40EA696BF87181E2 CRC64;

Query Match 18.2%; Score 4; DB 11; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 VES 15  
 ||||  
 Db 6 VES 9

RESULT 15  
 P81895  
 ID P81895 PRELIMINARY; PRT; 19 AA.  
 AC P81895;  
 DT 01-JUN-2000 (TREMBlrel. 14, Created)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE 2-OXOGLUTARATE DEHYDROGENASE (OGDC-E1) (FRAGMENT).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
 OC Solanales; Solanaceae; Solanum.  
 OX NCBI\_Taxid=4113;  
 RN [1]  
 RP  
 RC STRAIN-CV. ROMANO; TISSUE-TUBER;  
 RX MEDLINE=99441232; Pubmed=10510296;  
 RA Miller A.H., Hill S.A., Leaver C.J.;  
 RT "Plant mitochondrial 2-oxoglutarate dehydrogenase complex:  
 purification and characterization in potato.";  
 RL Biochem. J. 343:327-334(1999).  
 CC -1- FUNCTION: THE 2-OXOGLUTARATE DEHYDROGENASE COMPLEX CATALYZES THE  
 OVERALL CONVERSION OF 2-OXOGLUTARATE TO SUCCINYL-COA & CO(2). IT  
 CONTAINS MULTIPLE COPIES OF 3 ENZYMTIC COMPONENTS: 2-OXOGLUTARATE  
 DEHYDROGENASE (E1), DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (E2) AND  
 LIPOAMIDE DEHYDROGENASE (E3).  
 CC -1- CATALYTIC ACTIVITY: 2-OXOGLUTARATE + LIPOAMIDE = S-SUCCINYL-  
 DIHYDROLIPOAMIDE + CO(2).  
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.  
 DR InterPro: IPR000266; -;  
 DR ProDom: PD001295; -; 1.  
 KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;  
 KW Mitochondrion.  
 FT NON TER 19 19  
 SQ SEQUENCE 19 AA: 2022 MW: 3AB2C6910C61EEF7 CRC64;

Query Match 18.2%; Score 4; DB 10; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPV 12  
 ||||  
 Db 3 AAPV 6

Search completed: July 23, 2001, 17:06:07  
 Job time: 548 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 17:04:50 ; Search time 23.18 Seconds  
(without alignments)  
32.512 Million cell updates/sec

Title: US-09-351-296-16

Perfect score: 22

Sequence: 1 TATKQEAAPVYESKMTLEA 22

Scoring table: OLIGO

Searched: 93435 seqs, 34255486 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1176

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database: SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	27.3	13	1	PSAE_PEA
2	5	22.7	14	1	UHAI_CANFA
3	4	18.2	13	1	BLAC_STRGR
4	4	18.2	15	1	UC06_MAIZE
5	4	18.2	15	1	UN04_PIRNS
6	4	18.2	17	1	A45K_MTCBO
7	4	18.2	21	1	LE04_BIOGL
8	4	18.2	22	1	SETB_SALTY
9	3	13.6	8	1	CLP_THICU
10	3	13.6	9	1	DCML_PSECF
11	3	13.6	10	1	O20G_COMTE
12	3	13.6	13	1	CPI_APLCA
13	3	13.6	13	1	CXET_COMTE
14	3	13.6	13	1	FTBA_CAVPO
15	3	13.6	13	1	LIGA_TRAVE
16	3	13.6	13	1	LIGB_TRAVE
17	3	13.6	13	1	PSAU_PEA
18	3	13.6	13	1	PSBP_PIRNS
19	3	13.6	14	1	LPW_CITPR
20	3	13.6	14	1	LPW_ECOLI
21	3	13.6	14	1	LPW_SALTY
22	3	13.6	14	1	PH1_PRUSE
23	3	13.6	14	1	UC15_MAIZE
24	3	13.6	14	1	UN07_CLOPA
25	3	13.6	14	1	YMP2_XANCP
26	3	13.6	15	1	ATP2_SPIOL
27	3	13.6	15	1	ESTB_SCHGA
28	3	13.6	15	1	PH3_PRUSE
29	3	13.6	15	1	UC08_MAIZE
30	3	13.6	15	1	URE2_MORMO
31	3	13.6	16	1	FENR_STRGR
32	3	13.6	16	1	HTPG_ACICA
33	3	13.6	16	1	PH2_PRUSE

34	3	13.6	16	1	PSAJ_SPIOL	P17230 spinacia ol
35	3	13.6	17	1	GAST_BACIU	P33714 macaca mla
36	3	13.6	17	1	SP51_MACTI	P27642 bacillus li
37	3	13.6	17	1	VESP_VESMC	P57672 vesputia mac
38	3	13.6	18	1	NEA_BOVIN	P15506 bos taurus
39	3	13.6	19	1	ATPB_CANFA	P99504 comonomas t
40	3	13.6	19	1	DHAB_COMTE	P80704 rangifer ta
41	3	13.6	19	1	FIBA_RANFA	P14462 rangifer ta
42	3	13.6	19	1	H3_NARPS	P80553 narclissus p
43	3	13.6	19	1	HBB2_URCHA	P18992 utromastix h
44	3	13.6	19	1	HHP_THICU	P80487 thlobacillu
45	3	13.6	19	1	PHLC_STRAIN	P80924 staphylococ

## ALIGNMENTS

RESULT	ID	PSAE_PEA	STANDARD	PRT	13 AA.
AC	P20118:	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	01-JUL-1993 (Rel. 26, Last annotation update)				
DE	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV (PHOTOSYSTEM I 13 KDA PROTEIN) (PSI-E) (FRAGMENT).				
GN	PSAE.				
OS	Pisum sativum (Garden pea).				
OC	Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta: eudicotyledons: core eudicots: Rosidae; eurosids I;				
OC	Fabales; Fabaceae; Papilionoideae; Pisum.				
OX	NCBI_TaxID=3888;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=88137587; PubMed=3277857;				
RA	Dunn P.P.J., Packman L.C., Pappin D., Gray J.C.;				
RT	"N-terminal amino acid sequence analysis of the subunits of pea photosystem I."				
RL	FEBS Lett. 228:157-161(1988).				
CC	-I- FUNCTION: MAY FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.				
CC	-I- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE.				
CC	-I- SIMILARITY: BELONGS TO THE PSAE FAMILY.				
DR	PIR: S00316; S00316.				
KW	Photosynthesis; Photosystem I; Chloroplast; Thylakoid membrane.				
FT	NON_TER 13				
SO	SEQUENCE 13 AA; 1190 MW; D895A63A52D8DB1D CRC64;				
Query Match 27.3%; Score 6; DB 1; Length 13;					
Best local Similarity 100.0%; Pred. No. 3.1;					
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Oy	6 AEAAP 11				
Db	6 AEAAP 11				
RESULT 2					
UHAI_CANFA	STANDARD;				
AC	P99503;				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	15-JUL-1998 (Rel. 36, Last annotation update)				
DE	UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT 11) (FRAGMENT).				
OS	Canis familiaris (Dog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
OX	NCBI_TaxID=9615;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Heart;				

RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.3, ITS MW IS: 19.6 KDA.  
 DR HSC-2DPAGE; P95503; DOG.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1149 MW; 3D9238888D8668C7 CRC64;

Query Match 22.7%; Score 5; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAAAA 10  
 Db 1 AAAAA 5

RESULT 3  
 BLAC\_STRGR STANDARD; PRT; 13 AA.  
 AC P81173;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE BETA-LACTAMASE (EC 3.5.2.6) (FRAGMENT).  
 OS Streptomyces griseus.  
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 CC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1911;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=NRRL B-2682;  
 RX MEDLINE=98386507; PubMed=9720038;  
 RA Deak E., Szabo I., Kalmanchelyi A., Gal Z., Barabas G.,  
 RA Parvige A.;  
 RT "Membrane-bound and extracellular beta-lactamase production with  
 RT developmental regulation in Streptomyces griseus NRRL B-2682.";  
 RL Microbiology 144:2169-2177(1998).  
 CC -I- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)O = A SUBSTITUTED BETA-  
 CC AMINO ACID.  
 CC -I- SUBCELLULAR LOCATION: SECRETED AND MEMBRANE-BOUND.  
 CC -I- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.  
 DR InterPro: IPR000871;  
 DR PROSITE; PS00146; BETA-LACTAMASE\_A; PARTIAL.  
 KW Hydrolase; Antibiotic resistance; Membrane.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1236 MW; 14C512911BD54760 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAP 11  
 Db 1 AAAP 4

RESULT 4  
 UC06\_MAIZE STANDARD; PRT; 15 AA.  
 AC P80612;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 1131)  
 DE (FRAGMENT).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;  
 OC Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Toulzet P., Riccardi F., Morin C., Damerwal C., Huet J.-C.,  
 RA Penzlet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.8, ITS MW IS: 71.0 KDA.  
 DR Maize-2DPAGE; P80612; COLEOPTILE.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1390 MW; 7005E22830F23D61 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAP 11  
 Db 2 AAAP 5

RESULT 5  
 UN04\_PINPS STANDARD; PRT; 15 AA.  
 ID UN04\_PINPS  
 AC P81673;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N143) (FRAGMENT).  
 OS Pinus pinaster (Maritime pine).  
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 CC Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=71647;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Plombeau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomieu C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins.";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -I- INDUCTION: BY WATER-STRESS.  
 CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.2, ITS MW IS: 21 KDA.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1489 MW; CE4D85E9308227A CRC64;

Query Match 18.2%; Score 4; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EAAA 10  
 Db 6 EAAA 9

RESULT 6  
 A45K\_MYCBO STANDARD; PRT; 17 AA.  
 ID A45K\_MYCBO  
 AC P80069;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-OCT-1996 (Rel. 34, last annotation update)  
 DE 45/47 KDA ANTIGEN (FRAGMENT).  
 OS Mycobacterium bovis.  
 OC Bacteria: Firmicutes; Actinobacteria: Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1765;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=BCG / PARIS 1173 P2;  
 RX MEDLINE=93138802; PubMed=8423100;  
 RA Roman F., Laquerriere A., Miltzer P., Pescher P., Chavarot P.,  
 RA Lagraderie M., Auregan G., Gheorghiu M., Marchal G.A.;  
 RT "Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen  
 RT complex, an immunodominant target for antibody response after  
 RT immunization with living bacteria.";  
 RL Infect. Immun. 61:742-750(1993).  
 CC -1- SUBCELLULAR LOCATION: SECRETED.  
 CC -1- SIMILARITY: TO M.LEPRAE NL43, AND M.TUBERCULOSIS MPT32.  
 DR PIR: A49237; A49237.  
 KM Antigen.  
 FT NON\_TER  
 SO SEQUENCE 17 AA; 1521 MW; 4492CC389D9D9893 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AAP 11  
 DB 12 AAP 15

RESULT 7  
 LE04\_BIOGL STANDARD; PRT; 21 AA.  
 AC P80743;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, last sequence update)  
 DT 01-OCT-2000 (Rel. 40, last annotation update)  
 DE HEMOLYMPH 65 KDA LECTIN BG04 (FRAGMENT).  
 GN BG04.  
 OS Blomphalaria glabrata (Bloodfluke planorb).  
 OC Eukaryota: Metazoa: Mollusca: Gastropoda; Pulmonata; Basommatophora;  
 OC Planorbidae: Blomphalaria.  
 OX NCBI\_TaxID=6526;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=M-LINE; TISSUE=Hemolymph;  
 RX MEDLINE=97385165; PubMed=9238039;  
 RA Adema C.M., Hettel L.A., Miller R.D., Loker E.S.;  
 RT "A family of fibrinogen-related proteins that precipitates parasite-  
 RT derived molecules is produced by an invertebrate after infection.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:8691-8696(1997).  
 CC -1- FUNCTION: BINDS AND PRECIPITATES ANTIGENS OF THE PARASITE  
 CC ECHINOSTOMA PARANSEI.  
 CC -1- SUBCELLULAR LOCATION: SECRETED IN THE HEMOLYMPH.  
 CC -1- INDUCTION: BY INFECTION.  
 KM Lectin.  
 FT NON\_TER  
 FT NON\_TER  
 SO SEQUENCE 21 AA; 2239 MW; B8593D7A4902858C CRC64;

Query Match 18.2%; Score 4; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 VES 15  
 DB 13 VES 16

RESULT 8  
 SETB\_SALTY STANDARD; PRT; 22 AA.  
 AC P33027;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, last sequence update)  
 DT 01-OCT-2000 (Rel. 40, last annotation update)  
 DE SUGAR EFFLUX TRANSPORTER B (FRAGMENT).  
 GN SETB.  
 OS Salmonella typhimurium.  
 OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmoneilla.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89313694; PubMed=2546043;  
 RA Geerse R.H., Izzo F., Postma P.W.;  
 RT "The PEP: fructose phosphotransferase system in Salmonella  
 RT typhimurium: Fpr combines enzyme IIFru and pseudo-HPr activities.";  
 RL Mol. Gen. Genet. 216:517-525(1989).  
 CC -1- FUNCTION: INVOLVED IN THE EFFLUX OF SUGARS. THE PHYSIOLOGICAL ROLE  
 CC MAY BE THE DETOXIFICATION OF NON-METABOLIZABLE SUGAR ANALOGS. CAN  
 CC TRANSPORT LACTOSE AND GLUCOSE (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE  
 CC (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE SET FAMILY OF TRANSPORTERS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X14243; -; NOT ANNOTATED\_CDS.  
 DR StyGene: SG10423; setb.  
 KM Transport; Sugar transport; Transmembrane; Inner membrane.  
 FT TRANSMEM 13 >22 POTENTIAL.  
 FT NON\_TER 22  
 SO SEQUENCE 22 AA; 2291 MW; 2849C330172C5C2 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AAP 11  
 DB 7 AAP 10

RESULT 9  
 CLP\_THICU STANDARD; PRT; 8 AA.  
 AC P80488;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, last sequence update)  
 DT 01-OCT-1996 (Rel. 34, last annotation update)  
 DE CHEMOLITHOTROPH-SPECIFIC PROTEIN (FRAGMENT).  
 OS Thiobacillus cuprinus.  
 OC Bacteria: Proteobacteria; beta subdivision; Comamonadaceae; Thiomonas.  
 OX NCBI\_TaxID=36860;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=DSM 5494;  
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;  
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.  
 CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED  
 CC CHEMOLITHOTROPHICALLY.  
 FT NON\_TER 8  
 FT NON\_TER 8  
 SO SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match 13.6%; Score 3; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 APV 12  
 |||  
 Db 1 APV 3

RESULT 10  
 DCML\_PSECF STANDARD; PRT; 9 AA.  
 ID DCML\_PSECF  
 AC P19913;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DE 01-DEC-1992 (Rel. 24, Last annotation update)  
 OS CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).  
 CC Pseudomonas carboxydoflava.  
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;  
 CC Hydrogenophaga.  
 CC NCBI\_TaxID=47421;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90055678; PubMed=2818128;  
 RA Kreut M., Hugendieck I., Herwig S., Meyer O.;  
 RT "Homology and distribution of Co dehydrogenase structural genes in  
 RT carboxyotrophic bacteria.";  
 RL Arch. Microbiol. 152:335-341(1989).  
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED  
 CC ACCEPTOR.  
 CC -1- COFACTOR: MOLYBDENUM.  
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND  
 CC SMALL.  
 DR PIR; P10139; P10139.  
 KM Oxidoreductase; Molybdenum. N -> M.  
 FT VARIANT 2 2  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 974 MW; 0224DAB6C2D76DD4 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 APV 12  
 |||  
 Db 3 APV 5

RESULT 11  
 O2OG\_COMTE STANDARD; PRT; 10 AA.  
 ID O2OG\_COMTE  
 AC P80466; P80466.  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DE 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE QUINOLINE 2-OXIDOREDUCTASE, GAMMA CHAIN (EC 1.-.-.-) (FRAGMENT).  
 OS Comamonas testosteroni (Pseudomonas testosteroni).  
 CC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.  
 CC NCBI\_TaxID=285;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=63;  
 RX MEDLINE=96035889; PubMed=7556204;  
 RA Schach S., Teshisaka B., Fetzner S., Lingens F.;  
 RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-  
 RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in  
 RT quinoline and 3-methylquinoline degradation.";  
 RL Eur. J. Biochem. 232:536-544(1995).  
 CC -1- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-  
 CC 1,2-DIHYDROQUINOLINE.  
 CC -1- COFACTOR: FAD AND MOLYBDENUM.

CC -1- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND  
 CC (3-METHYL-)-QUINOLINE.  
 CC -1- SUBUNIT: HETEROPOLYMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND  
 CC TWO GAMMA CHAINS (PROBABLE).  
 KM Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1153 MW; C848CE64433B1DC6 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 QAE 7  
 |||  
 Db 3 QAE 5

RESULT 12  
 CPL\_APLCA STANDARD; PRT; 13 AA.  
 ID CPL\_APLCA  
 AC O10998;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE CEREBRAL PEPTIDE 1 (CPL).  
 OS Aplysia californica (California sea hare).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anasplidae;  
 CC Aplysiidae; Aplysia.  
 CC NCBI\_TaxID=6500;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=97001771; PubMed=8844763;  
 RA Phares G.A., Lloyd P.E.;  
 RT "Purification, primary structure, and neuronal localization of  
 RT cerebral peptide 1 from Aplysia.";  
 RL Peptides 17:753-761(1996).  
 CC -1- FUNCTION: MAY FUNCTION AS A PEPTIDE TRANSMITTER.  
 CC -1- TISSUE SPECIFICITY: FOUND PREDOMINANTLY IN THE CEREBRAL AND PEDAL  
 CC GANGLIA.  
 SQ SEQUENCE 13 AA; 1314 MW; 9DBC3CE82C667B05 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 LEA 22  
 |||  
 Db 11 LEA 13

RESULT 13  
 CXET\_COMTE STANDARD; PRT; 13 AA.  
 ID CXET\_COMTE  
 AC P81755;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE EPSILON-CONOTOXIN TXIX.  
 OS Conus textile (Cloth-of-gold cone).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 CC Neogastropoda; Conidae; Conidae; Conus.  
 CC NCBI\_TaxID=6494;  
 RN [1]  
 RP SEQUENCE, CARBOHYDRATE-LINKAGE SITE THR-10, AND STRUCTURE BY NMR.  
 RC TISSUE=Venom;  
 RX MEDLINE=99254114; PubMed=10318957;  
 RA Ribby A.C., Lucas-Neunier E., Kalume D.E., Czerwiatec E., Hambe B.,  
 RA Delguy I., Fossier P., Baux G., Roepstorff P., Baleja J.D.,  
 RA Furler B.C., Furler B., Stenflo J.P.;  
 RT "A conotoxin from Conus textile with unusual posttranslational



RT modifications reduces presynaptic  $Ca^{2+}$  influx \*;  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5758-5763(1999).  
 CC -1- FUNCTION: CONOTOXIN WHICH ACTS AT PRESYNAPTIC MEMBRANES, BLOCKING  
 THE CALCIUM CHANNELS.  
 CC -1- PIV: O-GLYCAN CONSISTS OF THE DISACCHARIDE GAL-GALNAc.  
 DR PDB: 1MCT; 08-JUN-99.  
 KW Presynaptic neurotoxin; Calcium channel inhibitor; Venom; Vitamin K;  
 KW Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Bromination;  
 KW 3D-structure.  
 KM DISULFID 2 8  
 FT DISULFID 3 9  
 FT MOD\_RES 1 1 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 4 4 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 7 7 BROMINATION.  
 FT MOD\_RES 13 13 HYDROXYLATION.  
 FT CARBOHYD 10 10 O-LINKED (GALNAc. . .).  
 SQ SEQUENCE 13 AA; 1388 MW; 386C9E1C74AF378 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAP 11  
 Db 11 AAP 13

RESULT 14  
 FIBA\_CAVPO STANDARD; PRT; 13 AA.  
 AC P1445:  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-JAN-1990 (Rel. 13, Last annotation update)  
 DE FIBRINOPEPTIDE A.  
 OS Cavia porcellus (Guinea pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Hystriognathii; Cavidae; Cavia.  
 OK NCBI\_TaxID=10141;  
 RN (1)  
 RP SEQUENCE.  
 RA Blomback B., Blomback M., Grondahl N.J.;  
 RT "Studies on fibrinopeptides from mammals.";  
 RL Acta Chem. Scand. 19:1789-1791(1965).  
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 AGGREGATION.  
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 KW Blood coagulation; Plasma.  
 KW NON\_TER 13  
 SQ SEQUENCE 13 AA; 1309 MW; 639999286C79DDDB CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAA 9  
 Db 6 EAA 8

RESULT 15  
 LIGA\_TRAVE STANDARD; PRT; 13 AA.  
 ID LIGA\_TRAVE  
 AC P20011;  
 DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE LIGNINASE A (EC 1.11.1.-) (LIGNIN PEROXIDASE) (FRAGMENT).  
 OS Trameetes versicolor (White-rot fungus).  
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Aphylliophorales;  
 CC Coriolaceae; Trameetes.  
 OK NCBI\_TaxID=5325;  
 RN (1)  
 RP SEQUENCE.  
 RX MEDLINE=89211432; PubMed=2707445;  
 RA Joensson L., Karlsson O., Lundquist K., Nyman P.O.;  
 RT "Trameetes versicolor ligninase: Isozyme sequence homology and  
 substrate specificity.";  
 RL FEBS Lett. 247:143-146(1989).  
 CC -1- CATALYTIC ACTIVITY: DEPOLYMERIZATION OF LIGNIN. CATALYZES THE  
 C(ALPHA)-C(BETA) CLEAVAGE OF THE PROPYL SIDE CHAINS OF LIGNIN.  
 CC -1- PATHWAY: FIRST STEP IN LIGNIN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. LIGNINASE SUBFAMILY.  
 DR PIR: S04013; S04013.  
 DR INTERPRO: IPR002016; .  
 DR PROSITE: PS00435; PEROXIDASE\_1; PARTIAL.  
 DR PROSITE: PS00436; PEROXIDASE\_2; PARTIAL.  
 KW Oxidoreductase; Peroxidase; Heme; Glycoprotein; Multigene family;  
 KW Lignin degradation.  
 KW NON\_TER 13  
 SQ SEQUENCE 13 AA; 1298 MW; 22C50ED5872A4338 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TAT 3  
 Db 9 TAT 11

Search completed: July 23, 2001, 17:04:50  
 Job time: 511 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:57:41 ; Search time 41.27 Seconds  
(without alignments)  
40.607 Million cell updates/sec

Title: US-09-351-296-16  
Perfect score: 22  
Sequence: 1 TATKQAEAAAPVESKMTLEA 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4035

Minimum DB seq length: 6  
Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :  
1: PIR\_68:\*  
2: pir1:\*  
3: pir2:\*  
4: pir3:\*  
5: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	27.3	13	2	S00316
2	5	22.7	12	2	PN0577
3	5	22.7	12	2	PN0578
4	5	22.7	12	2	PN0579
5	5	22.7	12	2	PN0580
6	5	22.7	12	2	PN0581
7	5	22.7	12	2	PN0576
8	5	22.7	15	2	PT0037
9	5	22.7	22	2	PC7072
10	4	18.2	10	2	PS0209
11	4	18.2	11	2	H54346
12	4	18.2	12	2	PO0696
13	4	18.2	13	2	A38929
14	4	18.2	15	2	PA0057
15	4	18.2	15	2	PO0692
16	4	18.2	15	2	PT0094
17	4	18.2	16	2	S36876
18	4	18.2	17	2	I55226
19	4	18.2	17	2	A49237
20	4	18.2	20	2	T01691
21	4	18.2	20	2	A42267
22	4	18.2	22	2	PO0667
23	4	18.2	22	2	D47256
24	3	13.6	6	2	B60110
25	3	13.6	6	2	JH0784
26	3	13.6	8	2	S68325
27	3	13.6	9	2	S66608
28	3	13.6	9	2	PL0139
29	3	13.6	9	2	A43848

30	3	13.6	9	2	B38740	Ig kappa chain C r
31	3	13.6	9	4	S15594	orf 1 para 5'-regl
32	3	13.6	10	2	C26697	unspecific monooxy
33	3	13.6	10	2	S69159	cystathionine gamm
34	3	13.6	10	2	PQ0783	NADH dehydrogenase
35	3	13.6	10	2	B61440	polysialacturonase
36	3	13.6	10	2	I52645	gene B-50 protein
37	3	13.6	10	2	C54226	light-harvesting P
38	3	13.6	11	2	PQ0682	photosystem I 17.5
39	3	13.6	11	2	PC4267	ribosomal protein
40	3	13.6	11	2	PN0167	ribosomal protein
41	3	13.6	11	2	PT0211	T-cell receptor al
42	3	13.6	11	4	S52252	hypothetical prote
43	3	13.6	12	2	A40763	sucrose-6-phosphat
44	3	13.6	12	2	PQ0776	NADH dehydrogenase
45	3	13.6	12	2	A28955	polysialoyllycoprol

#### ALIGNMENTS

RESULT 1  
S00316  
Photosystem I 13K protein - garden pea (fragment)  
C:Species: Pisum sativum (garden pea)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 18-Jun-1993  
C:Accession: S00316; P10019  
R:Dunn, P.P.U.; Packman, L.C.; Pappin, D.; Gray, J.C.  
FEBS Lett. 228, 157-161, 1988  
A:Title: N-terminal amino acid sequence analysis of the subunits of pea photosystem I  
A:Reference number: S00314; MUID:8817567  
A:Accession: S00316  
A:Molecule type: protein  
A:Residues: 1-13 <DUN>  
C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 27.3% Score 6; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AEAAP 11  
Db 6 AEAAP 11

RESULT 2  
PN0577  
tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - gorilla (fragment)  
N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase  
C:Species: Gorilla gorilla (gorilla)  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000  
C:Accession: PN0577  
R:Richmose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Negatsu, T.  
Biochem. Biophys. Res. Commun. 195, 158-165, 1993  
A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.  
A:Reference number: PN0575; MUID:93371398  
A:Accession: PN0577  
A:Molecule type: genomic RNA  
A:Residues: 1-12 <ICH>  
A:Cross-references: GB:I14795  
A:Experimental source: lymphocytes of peripheral blood  
C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine bi  
C:Superfamily: phenylalanine 4-monooxygenase  
C:Keywords: bipterin; monooxygenase; oxidoreductase

Query Match 22.7% Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KOAEA 8  
Db 4 KOAEA 8

Db 6 KQAEA 10

RESULT 3

PN0578

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - orangutan (fragment)

N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase

C:Species: Pongo pygmaeus (orangutan)

C>Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000

C:Accession: PN0578

R:Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.

Biochem. Biophys. Res. Commun. 195, 158-165, 1993

A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.

A:Reference number: PN0575; MUID:93371398

A:Accession: PN0578

A:Molecule type: genomic RNA

A:Residues: 1-12 <ICH>

A:Cross-references: GB:L14798

A:Experimental source: lymphocytes of peripheral blood

C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis

C:Superfamily: phenylalanine 4-monooxygenase

C:Keywords: bioperin; monooxygenase; oxidoreductase

Query Match 22.7%; Score 5; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KQAEA 8

|||||

Db 6 KQAEA 10

RESULT 4

PN0579

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - common gibbon (fragment)

N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase

C:Species: Hylobates lar (common gibbon, white-handed gibbon)

C>Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000

C:Accession: PN0579

R:Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.

Biochem. Biophys. Res. Commun. 195, 158-165, 1993

A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.

A:Reference number: PN0575; MUID:93371398

A:Accession: PN0579

A:Molecule type: genomic RNA

A:Residues: 1-12 <ICH>

A:Cross-references: GB:L14792

A:Experimental source: lymph nodes

C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis

C:Superfamily: phenylalanine 4-monooxygenase

C:Keywords: bioperin; monooxygenase; oxidoreductase

Query Match 22.7%; Score 5; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KQAEA 8

|||||

Db 6 KQAEA 10

RESULT 5

PN0580

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - Japanese macaque (fragment)

N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase

C:Species: Macaca fuscata (Japanese macaque)

C>Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000

C:Accession: PN0580

R:Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.

Biochem. Biophys. Res. Commun. 195, 158-165, 1993

A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.

A:Reference number: PN0575; MUID:93371398

A:Accession: PN0580

A:Molecule type: genomic RNA

A:Residues: 1-12 <ICH>

A:Cross-references: GB:L14804

A:Experimental source: kidney

C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis

C:Superfamily: phenylalanine 4-monooxygenase

C:Keywords: bioperin; monooxygenase; oxidoreductase

Query Match 22.7%; Score 5; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KQAEA 8

|||||

Db 6 KQAEA 10

RESULT 6

PN0581

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - common marmoset (fragment)

N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase

C:Species: Callithrix jacchus (common marmoset)

C>Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000

C:Accession: PN0581

R:Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.

Biochem. Biophys. Res. Commun. 195, 158-165, 1993

A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.

A:Reference number: PN0575; MUID:93371398

A:Accession: PN0581

A:Molecule type: genomic RNA

A:Residues: 1-12 <ICH>

A:Cross-references: GB:L14803

A:Experimental source: kidney

C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis

C:Superfamily: phenylalanine 4-monooxygenase

C:Keywords: bioperin; monooxygenase; oxidoreductase

Query Match 22.7%; Score 5; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KQAEA 8

|||||

Db 6 KQAEA 10

RESULT 7

PN0576

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - chimpanzee (fragment)

N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase

C:Species: Pan troglodytes (chimpanzee)

C>Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000

C:Accession: PN0576

R:Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.

Biochem. Biophys. Res. Commun. 195, 158-165, 1993

A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.

A:Reference number: PN0575; MUID:93371398

A:Accession: PN0576

A:Molecule type: genomic RNA

A:Residues: 1-12 <ICH>

A:Cross-references: GB:L14789

A:Experimental source: lymphocytes of peripheral blood

C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis

C:Superfamily: phenylalanine 4-monooxygenase

C:Keywords: bioperin; monooxygenase; oxidoreductase

Query Match 22.7%; Score 5; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 KOAEA 8  
 |||||  
 Db 6 KOAEA 10

RESULT 8  
 PT0037  
 light harvesting complex chain III/b, photosystem I - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993  
 C:Accession: PT0037; PS0205  
 R:Uchiyama, Y.; Tsugita, A.  
 Submitted to JIPID, June 1991  
 A:Reference number: PS0189  
 A:Accession: PT0037  
 A:Molecule type: protein  
 A:Residues: 1-15 <UCH>

Query Match 22.7%; Score 5; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EAAAP 11  
 |||||  
 Db 4 EAAAP 8

RESULT 9  
 PC7072  
 H+-transporting ATP synthase (EC 3.6.1.34) delta chain, mitochondrial - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
 C:Accession: PC7072  
 R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;  
 Electrophoresis 21, 1853-1871, 2000  
 A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of  
 A:Reference number: PC7072  
 A:Accession: PC7072  
 A:Molecule type: protein  
 A:Residues: 1-22 <TSU>  
 A:Experimental source: strain C57BL/6Cr SLC, male; brain, striatum  
 C:Keywords: brain; hydrolase; mitochondrion

Query Match 22.7%; Score 5; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAAA 10  
 |||||  
 Db 1 AEAAA 5

RESULT 10  
 PS0209  
 24K protein 4407 - rice (strain Nihonbare) (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
 C:Accession: PS0209  
 R:Tsugita, A.; Kamo, M.  
 Submitted to JIPID, April 1993  
 A:Reference number: PS0209  
 A:Accession: PS0209  
 A:Molecule type: protein  
 A:Residues: 1-10 <TSU>  
 A:Experimental source: callus  
 C:Comment: molecular weight 24K, pI 4.6.

Query Match 18.2%; Score 4; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAA 9  
 |||||  
 Db 7 AEAA 10

RESULT 11  
 H54346  
 pyruvate synthase (EC 1.2.7.1) alpha chain - Pyrococcus furiosus (fragment)  
 C:Species: Pyrococcus furiosus  
 C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-May-2000  
 C:Accession: H54346  
 R:Blamey, J.M.; Adams, M.W.  
 Biochemistry 33, 1000-1007, 1994  
 A:Title: Characterization of an ancestral type of pyruvate ferredoxin oxidoreductase  
 A:Reference number: A54346; MUID:94137707  
 A:Accession: H54346  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-11 <BLA>  
 C:Keywords: coenzyme A; oxidoreductase

Query Match 18.2%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EAAA 10  
 |||||  
 Db 7 EAAA 10

RESULT 12  
 PQ0696  
 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) [Imported] - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C:Accession: PQ0696  
 R:Komatsu, S.; Kajiwara, H.; Hirano, H.  
 Theor. Appl. Genet. 86, 935-942, 1993  
 A:Title: A rice protein library: a data-file of rice proteins separated by two-dimens  
 A:Reference number: PQ0696  
 A:Accession: PQ0696  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <KOM>  
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 18.2%; Score 4; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EAAA 10  
 |||||  
 Db 1 EAAA 4

RESULT 13  
 A38929  
 glutathione peroxidase (EC 1.11.1.9) - sheep (fragment)  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 31-Oct-1997  
 C:Accession: A38929  
 R:Gettings, P.; Dyal, D.; Crews, B.  
 Arch. Biochem. Biophys. 294, 511-518, 1992  
 A:Title: Selenium-dependent glutathione peroxidases from ovine and bovine erythrocyte  
 A:Reference number: S21712; MUID:92231574  
 A:Accession: A38929  
 A>Status: preliminary  
 A:Molecule type: protein

A:Residues: 1-13 <GET>  
 C:Superfamily: glutathione peroxidase  
 C:Keywords: oxidoreductase

Query Match 18.2%; Score 4; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 AAP 11  
 ||||  
 Db 7 AAP 10

## RESULT 14

P00692  
 Photosystem I 18.5K D2 chain - tobacco (Nicotiana tomentosiformis) (fragment)  
 C:Species: Nicotiana tomentosiformis  
 C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
 C:Accession: P00692  
 R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiyura, M.  
 Plant Physiol. 102, 1259-1267, 1993  
 A:Title: Molecular heterogeneity of photosystem I. psad, psaf, psah and psal are a  
 A:Reference number: P00667; MUID:94105345  
 A:Accession: P00692  
 A:Molecule type: protein  
 A:Residues: 1-15 <OBO>  
 A:Superfamily: photosystem I chain II  
 C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 18.2%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 EAA 10  
 ||||  
 Db 3 EAA 6

## RESULT 15

PA0057  
 adenylylate isopentenyltransferase (EC 2.5.1.27) - fungus (Fusarium sporotrichioides) (fra  
 C:Species: Fusarium sporotrichioides  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0057  
 R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi  
 A:Reference number: PA0051  
 A:Accession: PA0057  
 A:Molecule type: protein  
 A:Residues: 1-15 <CHO>  
 C:Keywords: transferase

Query Match 18.2%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 AAP 11  
 ||||  
 Db 1 AAP 4

Search completed: July 23, 2001, 16:57:41  
 Job time: 283 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:56:53 ; Search time 34.6 Seconds  
(Without alignments)  
12.809 Million cell updates/sec

Title: US-09-351-296-16

Sequence: 1 TATKQAEAAAPVESKMTLEA 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 193259 seqs, 20144635 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93443

Minimum DB seq length: 6  
Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/iaa/PCUTS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	2	US-08-845-926-16 Sequence 16, Appl
2	18	81.8	22	2	US-08-845-926-13 Sequence 13, Appl
3	5	22.7	6	2	US-08-793-490-2 Sequence 2, Appl
4	5	22.7	7	2	US-08-630-645-25 Sequence 25, Appl
5	5	22.7	7	5	PCT-US6-10220-25 Sequence 25, Appl
6	5	22.7	9	2	US-08-658-639-3 Sequence 3, Appl
7	5	22.7	9	4	US-08-944-604-3 Sequence 3, Appl
8	5	22.7	12	1	US-08-176-500-15 Sequence 15, Appl
9	5	22.7	12	1	US-08-471-052A-15 Sequence 15, Appl
10	5	22.7	12	1	US-08-381-960-9 Sequence 15, Appl
11	5	22.7	12	1	US-08-189-331-15 Sequence 15, Appl
12	5	22.7	12	2	US-08-471-939-15 Sequence 15, Appl
13	5	22.7	12	2	US-08-471-800-15 Sequence 15, Appl
14	5	22.7	12	2	US-08-471-068-15 Sequence 15, Appl
15	5	22.7	12	2	US-08-630-645-24 Sequence 15, Appl
16	5	22.7	12	5	PCT-US96-10220-24 Sequence 24, Appl
17	5	22.7	13	2	US-08-632-514C-25 Sequence 25, Appl
18	5	22.7	13	3	US-09-188-177-25 Sequence 25, Appl
19	5	22.7	14	1	US-08-340-203A-14 Sequence 14, Appl
20	5	22.7	14	3	US-09-085-407-14 Sequence 14, Appl
21	5	22.7	16	2	US-08-660-592-3 Sequence 3, Appl
22	5	22.7	16	2	US-08-660-592-8 Sequence 3, Appl
23	5	22.7	16	4	US-09-166-930A-3 Sequence 3, Appl
24	5	22.7	17	1	US-07-591-988B-1 Sequence 1, Appl
25	5	22.7	17	1	US-07-591-988B-2 Sequence 2, Appl
26	5	22.7	17	1	US-07-591-988B-3 Sequence 3, Appl
27	5	22.7	17	1	US-07-591-988B-3 Sequence 3, Appl

28	5	22.7	17	1	US-07-591-988B-4 Sequence 4, Appl
29	5	22.7	17	1	US-07-591-988B-5 Sequence 5, Appl
30	5	22.7	17	1	US-08-164-618-2 Sequence 2, Appl
31	5	22.7	17	1	US-08-164-618-3 Sequence 3, Appl
32	5	22.7	17	1	US-08-164-618-4 Sequence 4, Appl
33	5	22.7	17	1	US-08-006-037-1 Sequence 1, Appl
34	5	22.7	17	1	US-08-006-037-2 Sequence 2, Appl
35	5	22.7	17	1	US-08-006-037-3 Sequence 3, Appl
36	5	22.7	17	1	US-08-006-037-4 Sequence 4, Appl
37	5	22.7	17	1	US-08-006-037-5 Sequence 5, Appl
38	5	22.7	17	2	US-08-955-206-4 Sequence 4, Appl
39	5	22.7	17	2	US-08-614-377A-11 Sequence 11, Appl
40	5	22.7	17	3	US-08-955-050-4 Sequence 4, Appl
41	5	22.7	17	4	US-09-142-648B-11 Sequence 11, Appl
42	5	22.7	19	2	US-08-660-592-4 Sequence 4, Appl
43	5	22.7	19	2	US-08-660-592-5 Sequence 5, Appl
44	5	22.7	19	4	US-09-166-930A-4 Sequence 4, Appl
45	5	22.7	19	4	US-09-166-930A-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-08-845-926-16  
Sequence 16, Application US/08845926  
Patent No. 5935778  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike  
APPLICANT: SCHMITT, Urban  
APPLICANT: JUNG, G nther-Gerhard  
APPLICANT: IHLENFELDT, HANS-Georg  
APPLICANT: KRAAS, Wolfgang  
TITLE OF INVENTION: Method for serological typing using  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845,926  
FILING DATE: 04-28-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/598,993  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 04 302.2  
FILING DATE: 09-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:

ORGANISM: Hepatitis C Virus  
US-08-845-926-16

Query Match 100.0%; Score 22; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 9.7e-16;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TATKQAEAAAPVYESKRWLEA 22  
|||||  
Db 1 TATKQAEAAAPVYESKRWLEA 22

RESULT 2  
US-08-845-926-13  
Sequence 13, Application US/08845926  
Patent No. 5935778  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike  
APPLICANT: SCHMITT, Urban  
APPLICANT: JUNG, G nther-Gerhard  
APPLICANT: IHLENFELDT, HANS-Georg  
TITLE OF INVENTION: Method for serological typing using  
TITLE OF INVENTION: type-specific antigens  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845,926  
FILING DATE: 04-28-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/598,993  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA: DE 195 04 302.2  
APPLICATION NUMBER: DE 195 04 302.2  
FILING DATE: 09-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Hepatitis C Virus  
US-08-845-926-13

Query Match 81.8%; Score 18; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 8.2e-12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TATKQAEAAAPVYESKRW 18  
|||||

Db 1 TATKQAEAAAPVYESKRW 18

RESULT 3  
US-08-793-490-2  
Sequence 2, Application US/08793490  
Patent No. 5968824  
GENERAL INFORMATION:  
APPLICANT: Spruce, Barbara A  
APPLICANT: Prescott, Alan  
APPLICANT: Bolliger, Angelika  
APPLICANT: Dewar, Deborah A  
TITLE OF INVENTION: Agents for Inducing Apoptosis and Applications of Said  
TITLE OF INVENTION: Agents in Therapy  
FILE REFERENCE: ME A9701  
CURRENT APPLICATION NUMBER: US/08/793,490  
CURRENT FILING DATE: 1997-04-28  
EARLIER APPLICATION NUMBER: GB 9419285.3  
EARLIER FILING DATE: 1994-09-23  
EARLIER APPLICATION NUMBER: GB 9417444.8  
EARLIER FILING DATE: 1994-08-30  
EARLIER APPLICATION NUMBER: PCT/GB95/02037  
EARLIER FILING DATE: 1995-08-30  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: sequence  
OTHER INFORMATION: encoded by anti-proenkephalin immunoglobulin heavy  
US-08-793-490-2

Query Match 22.7%; Score 5; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 RTLEA 22  
|||||  
Db 2 RTLEA 6

RESULT 4  
US-08-630-645-25  
Sequence 25, Application US/08630645  
Patent No. 5948763  
GENERAL INFORMATION:  
APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
APPLICANT: FRANGIONE, Blas  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEWMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,645  
FILING DATE:  
CLASSIFICATION: 530



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-630-645-25

Query Match 22.7%; Score 5; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPV 13  
|||||  
DB 1 AAPV 5

RESULT 5  
PCT-US96-10220-25  
Sequence 25, Application PC/TUS9610220  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10220

FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

PCT-US96-10220-25

Query Match 22.7%; Score 5; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPV 13  
|||||  
DB 1 AAPV 5

RESULT 6  
US-08-658-639-3  
Sequence 3, Application US/08658639  
Patent No. 5914238  
GENERAL INFORMATION:

APPLICANT: KEESEE, SUSAN  
APPLICANT: OBAR, ROBERT  
APPLICANT: WU, YING-JYE

TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF  
TITLE OF INVENTION: BREAST CANCER  
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA

COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,639  
FILING DATE:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MEYERS, THOMAS C  
REGISTRATION NUMBER: 36,989  
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-658-639-3

Query Match 22.7%; Score 5; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAAAA 10  
|||||  
DB 2 AAAAA 6

RESULT 7  
US-08-944-604-3  
Sequence 3, Application US/08944604  
Patent No. 6218131

GENERAL INFORMATION:  
APPLICANT: KEESEE, SUSAN  
APPLICANT: OBAR, ROBERT  
APPLICANT: WU, YING-JYE

;; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF  
;; TITLE OF INVENTION: BREAST CANCER  
;; NUMBER OF SEQUENCES: 24  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Testa, Hurwitz & Thibault  
;; STREET: 125 High St.  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02110  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/944,604  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MEYERS, THOMAS C  
;; REGISTRATION NUMBER: 36,989  
;; REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 248-7000  
;; TELEFAX: (617) 248-7100  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-944-604-3

Query Match 22.7%; Score 5; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAAAA 10  
|||||  
Db 2 AAAAA 6

RESULT 8  
US-08-176-500-15  
;; Sequence 15, Application US/08176500  
;; Patent No. 5498538  
;; GENERAL INFORMATION:  
;; APPLICANT: Kay, B. K.  
;; APPLICANT: Fowlkes, D. M.  
;; TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
;; NUMBER OF SEQUENCES: 141  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Pennie & Edmonds  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10036-2711  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/176,500  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/013,416  
;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mistrock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-143  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212 790-9090  
;; TELEFAX: 212 869-8864/9741  
;; TELE: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; US-08-176-500-15

Query Match 22.7%; Score 5; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAAAA 10  
|||||  
Db 7 AAAAA 11

RESULT 9  
US-08-471-052A-15  
;; Sequence 15, Application US/08471052A  
;; Patent No. 5625033  
;; GENERAL INFORMATION:  
;; APPLICANT: Kay, B. K.  
;; APPLICANT: Fowlkes, D. M.  
;; TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
;; NUMBER OF SEQUENCES: 16  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Pennie & Edmonds  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10036-2711  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/471,052A  
;; FILING DATE: 06-JUNE-1995  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mistrock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-179  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212 790-9090  
;; TELEFAX: 212 869-8864/9741  
;; TELE: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; US-08-471-052A-15

Query Match 22.7%; Score 5; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEAAA 10  
Db 7 AEAAA 11

RESULT 10  
US-08-381-960-9  
; Sequence 9, Application US/08381960  
; Patent No. 5723287  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Improvements in or relating to  
; TITLE OF INVENTION: recombinant viruses  
; NUMBER OF SEQUENCES: 10  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,960  
; FILING DATE:  
; CLASSIFICATION: 514  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: Internal  
US-08-381-960-9

Query Match 22.7%; Score 5; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAAAP 11  
Db 4 EAAAP 8

RESULT 11  
US-08-189-331-15  
; Sequence 15, Application US/08189331  
; Patent No. 5747334  
; GENERAL INFORMATION:  
; APPLICANT: Kay, B. K.  
; APPLICANT: Fowlkes, D. M.  
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
; NUMBER OF SEQUENCES: 186  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennile & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/189,331  
; FILING DATE: Concurrently herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-189-331-15

Query Match 22.7%; Score 5; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEAAA 10  
Db 7 AEAAA 11

RESULT 12  
US-08-471-939-15  
; Sequence 15, Application US/08471939  
; Patent No. 5844076  
; GENERAL INFORMATION:  
; APPLICANT: Kay, B. K.  
; APPLICANT: Fowlkes, D. M.  
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennile & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,939  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/013,416  
; FILING DATE: 01-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-143  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-471-939-15

Query Match 22.7%; Score 5; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAAAA 10  
|11111  
Db 7 AAAAA 11

## RESULT 13

US-08-471-800-15  
; Sequence 15, Application US/08471800  
; Patent No. 5852167  
; GENERAL INFORMATION:  
; APPLICANT: Kay, B. K.  
; APPLICANT: Fowlkes, D. M.  
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,800  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/013,416  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-143  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-471-800-15

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAAAA 10  
|11111  
Db 7 AAAAA 11

## RESULT 14

US-08-471-068-15  
; Sequence 15, Application US/08471068  
; Patent No. 5948635  
; GENERAL INFORMATION:  
; APPLICANT: Kay, B. K.  
; APPLICANT: Fowlkes, D. M.  
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
; NUMBER OF SEQUENCES: 186  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,068  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/189,331  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-068-15

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAAAA 10  
|11111  
Db 7 AAAAA 11

## RESULT 15

US-08-630-645-24  
; Sequence 24, Application US/08630645  
; Patent No. 5948763  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,645  
; FILING DATE:  
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-630-645-24

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 9 AAPV 13  
| | | | |  
Db 5 AAPV 9

Search completed: July 23, 2001, 16:56:53  
Job time: 270 sec.

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:56:13 ; Search time 65.41 Seconds  
(Without alignments)  
20.390 Million cell updates/sec

Title: US-09-351-296-16

Perfect score: 22

Sequence: 1 TATKQEAAPVESHKMTLEA 22

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 148088

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

A\_Geneseq\_0601:\*

1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:\*

2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:\*

3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:\*

4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:\*

5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:\*

6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:\*

7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT:\*

8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT:\*

9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT:\*

10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:\*

11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:\*

12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:\*

13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:\*

14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:\*

15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:\*

16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:\*

17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:\*

18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:\*

19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:\*

20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:\*

21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:\*

22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	17	AA999906 Hepatitis C Virus
2	18	81.8	22	17	AA999903 Hepatitis C Virus
3	10	45.5	22	17	AA995548 Hepatitis C Virus
4	9	40.9	9	17	AA449321 Human leucocyte an
5	8	36.4	11	17	AA449276 Human leucocyte an
6	5	22.7	7	18	AA432550 Anti-prion peptide
7	5	22.7	8	21	AA837838 Neisserial conserv
8	5	22.7	9	19	AA444355 Breast cancer-asso
9	5	22.7	11	17	AA968835 Human neurofilamen
10	5	22.7	12	15	AA851235 Part of pNTPenv in
11	5	22.7	12	18	AAW32549 Anti-prion peptide

12	5	22.7	13	19	AAW38350 Apoptosis associat
13	5	22.7	15	21	AAV82047 MHC class II prote
14	5	22.7	15	21	AAV82059 MHC class II prote
15	5	22.7	15	21	AAV82062 MHC class II prote
16	5	22.7	15	21	AAV82063 MHC class II prote
17	5	22.7	15	21	AAV82073 MHC class II prote
18	5	22.7	15	21	AAV88958 Copeptide useful f
19	5	22.7	15	21	AAV88970 Copeptide useful f
20	5	22.7	15	21	AAV88973 Copeptide useful f
21	5	22.7	15	21	AAV88974 Copeptide useful f
22	5	22.7	15	21	AAV88981 Copeptide useful f
23	5	22.7	16	19	AAW41505 Heparin binding pe
24	5	22.7	16	21	AAV87838 Heparin binding pe
25	5	22.7	17	13	AAAR3625 Metallopolypeptide
26	5	22.7	17	13	AAAR3626 Metallopolypeptide
27	5	22.7	17	13	AAAR3627 Metallopolypeptide
28	5	22.7	17	18	AAW37493 Synthetic cadmium
29	5	22.7	17	20	AAV05337 Target sequence pe
30	5	22.7	17	21	AAAR20848 Peptide amino acid
31	5	22.7	19	21	AAV87834 Heparin binding pe
32	5	22.7	19	21	AAV87835 Heparin binding pe
33	5	22.7	22	16	AAAR73960 Duffy blood group
34	4	18.2	6	18	AAAR83196 Hexapeptide having
35	4	18.2	6	21	AAAR26566 Peptide immunoreac
36	4	18.2	6	21	AAV76876 Transforming growt
37	4	18.2	7	15	AAV16800 Peptide h2N-1p-Glu
38	4	18.2	7	15	AAAR52675 Fragment encoded b
39	4	18.2	7	16	AAAR84117 Equine herpesvirus
40	4	18.2	7	19	AAW44923 Negative control s
41	4	18.2	7	20	AAV42884 Vpr-binding peptid
42	4	18.2	7	21	AAAB4456 Sterile alpha moti
43	4	18.2	7	22	AAAB9447 Mannanase peptide
44	4	18.2	8	9	AAAB1972 Novel peptide subs
45	4	18.2	8	13	AAAR28332 Antigenic syntheti

#### ALIGNMENTS

RESULT 1	
AA999906	standard; peptide: 22 AA.
XX	
AC	AA999906;
XX	
DT	23-APR-1997 (first entry)
XX	
DE	Hepatitis C Virus antigen peptide 16.
XX	
KW	HCV; immunologically reactive; antigen; epitope; screen; typing;
KW	antibody; Immobilised.
XX	
OS	Hepatitis C Virus.
XX	
PN	EP726463-AZ.
XX	
PD	14-AUG-1996.
XX	
PF	09-FEB-1996; 96EP-0101925.
XX	
PR	09-FEB-1995; 95DE-4004302.
XX	
PA	(BOEP ) BOEHRINGER MANNHEIM GMBH.
XX	
PI	Schmitt U, Seidel C, Wlenhues-theilen U;
XX	
DR	WPI; 1996-364504/37.
XX	
PT	Antibody typing by sequential reaction with immobilised antigens -
PT	esp. using new hepatitis C virus peptide(s) as antigens
XX	
PS	Claim 9; Page 14; 22pp; German.
XX	

CC AAR9891-920 comprise at least one immunologically active region of  
CC hepatitis C virus (HCV), selected from amino acid sequences 384-414,  
CC 1738-1759, 2217-2236, 2402-2419 and 2345-2357. The peptides are  
CC used in a claimed method for typing antibodies in a 11q. sample.  
CC Assays performed using the peptides as antigens, which corresp. to  
CC regions of high immunogenicity and variability, can be performed  
CC routinely using simple equipment to provide accurate HCV typing.  
CC AAR9901-06 are derived from amino acids 1738-1759 of the NS4-region  
CC of HCV.  
XX  
XX  
SQ Sequence 22 AA;  
  
Query Match 100.0%; Score 22; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.1e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TATKQAEAAAPVSESKWRTLEA 22  
Db 1 tatkgaeaaapveskwrtleaa 22  
|||||  
|  
  
RESULT 2  
AAR9903 standard; peptide: 22 AA.  
XX  
XX AAR9903;  
XX  
XX 23-APR-1997 (first entry)  
XX  
XX Hepatitis C Virus antigen peptide 13.  
XX  
XX HCV; immunologically reactive; antigen; epitope; screen; typing;  
XX antibody; immobilised.  
XX  
XX Hepatitis C Virus.  
XX  
XX EP726463-A2.  
XX  
XX 14-AUG-1996.  
XX  
XX 09-FEB-1996; 96EP-0101925.  
XX  
XX 09-FEB-1995; 95DE-4004302.  
XX  
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX  
XX Schmitt U, Seidel C, Wienhues-thejen U;  
XX  
XX WPI: 1996-364504/37.  
XX  
XX  
XX Antibody typing by sequential reaction with immobilised antigens -  
XX esp. using new hepatitis C virus peptide(s) as antigens  
XX  
XX Claim 9; Page 14; 22pp; German.  
XX  
XX  
CC AAR9891-920 comprise at least one immunologically active region of  
CC hepatitis C virus (HCV), selected from amino acid sequences 384-414,  
CC 1738-1759, 2217-2236, 2402-2419 and 2345-2357. The peptides are  
CC used in a claimed method for typing antibodies in a 11q. sample.  
CC Assays performed using the peptides as antigens, which corresp. to  
CC regions of high immunogenicity and variability, can be performed  
CC routinely using simple equipment to provide accurate HCV typing.  
CC AAR9901-06 are derived from amino acids 1738-1759 of the NS4-region  
CC of HCV.  
XX  
XX  
SQ Sequence 22 AA;  
  
Query Match 81.8%; Score 18; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATKQAEAAAPVSESKWR 18  
Db 1 tatkgaeaaapveskwrt 18  
|||||  
|  
  
RESULT 3  
AAR9548 standard; Peptide: 22 AA.  
XX  
XX AAR9548;  
XX  
XX 26-SEP-1996 (first entry)  
XX  
XX Hepatitis C Virus I Non-Structural protein 4 epitope.  
XX  
XX HCV; hepatitis C virus; epitope; antigen; detection; chimera.  
XX  
XX Hepatitis C virus.  
XX  
XX JP08073497-A.  
XX  
XX 19-MAR-1996.  
XX  
XX 31-AUG-1994; 94JP-0232073.  
XX  
XX 31-AUG-1994; 94JP-0232073.  
XX  
XX (TOFU ) TONEN CORP.  
XX  
XX WPI: 1996-205533/21.  
XX  
XX New hepatitis C virus chimeric antigenic peptide - for the detection  
XX of hepatitis C virus infection or its group  
XX  
XX Claim 4; Page 14; 15pp; Japanese.  
XX  
XX The present sequence is that of a group I hepatitis C virus (HCV)  
XX non-structural protein 4 (NS4) epitope, designated 1-Y. Chimeras  
XX prepared by connecting at least two different epitopes on the group I  
XX HCV-related antigen, encoded by the genomic RNA of HCV or its cDNA,  
XX through a peptide linkage, are useful for the specific detection of  
XX HCV infection.  
XX  
XX Sequence 22 AA;  
  
Query Match 45.5%; Score 10; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.0035;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TATKQAEAAA 10  
Db 13 tatkgaeaaa 22  
|||||  
|  
  
RESULT 4  
AAW49321 standard; peptide: 9 AA.  
XX  
XX AAW49321;  
XX  
XX 05-JUN-1998 (first entry)  
XX  
XX Human leucocyte antigen DQ4 binding peptide #212.  
XX  
XX Human leucocyte antigen; HLA-DQ4; combinatorial library;  
XX autoimmune disease; chronic articular rheumatism.  
XX  
XX Synthetic.  
XX  
XX JP08151396-A.  
XX  
XX 11-JUN-1996.



XX 28-NOV-1994; 94JP-0292657.  
 PF Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 PR 28-NOV-1994; 94JP-0292657.  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX (TEIJ ) TEIJIN LTD.  
 PA WPI; 1996-329479/33.  
 XX HLA-binding oligopeptide and an immuno:regulator contg it - used in  
 PT the treatment of auto:immune disease  
 PS Claim 4; Page 30; 61pp: Japanese.  
 XX This peptide is an example of a peptide which binds to a human leucocyte  
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid  
 CC combinatorial library comprising the sequence AAV05953, by screening  
 CC with an HLA-DQ4 molecule. The peptide is used for the treatment of  
 CC autoimmune disease, or especially for treatment of viral diseases.  
 XX Sequence 9 AA;  
 SQ

Query Match 40.9%; Score 9; DB 17; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 APVYESKWR 18  
 DB 1 apvyeskwr 9

RESULT 5  
 AAW49276 ID AAW49276 standard; peptide: 11 AA.  
 XX AAW49276;  
 XX 05-JUN-1998 (first entry)  
 DE Human leucocyte antigen DQ4 binding peptide #167.  
 XX Human leucocyte antigen; HLA-DQ4; combinatorial library;  
 KM autoimmune disease; chronic articular rheumatism.  
 XX Synthetic.  
 OS JP08151396-A.  
 PN 11-JUN-1996.  
 PD 28-NOV-1994; 94JP-0292657.  
 PF 28-NOV-1994; 94JP-0292657.  
 XX 28-NOV-1994; 94JP-0292657.  
 XX (TEIJ ) TEIJIN LTD.  
 PA WPI; 1996-329479/33.  
 XX HLA-binding oligopeptide and an immuno:regulator contg it - used in  
 PT the treatment of auto:immune disease  
 PS Claim 4; Page 26; 61pp: Japanese.  
 XX This peptide is an example of a peptide which binds to a human leucocyte  
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid  
 CC combinatorial library comprising the sequence AAV05953, by screening  
 CC with an HLA-DQ4 molecule. The peptide is used for the treatment of  
 CC autoimmune disease, or especially for treatment of viral diseases.  
 XX Sequence 11 AA;  
 SQ

Query Match 36.4%; Score 8; DB 17; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 AAPVYES 15  
 DB 1 aapvyes 8

RESULT 6  
 AAW32550 ID AAW32550 standard; peptide: 7 AA.  
 XX AAW32550;  
 AC 21-JAN-1998 (first entry)  
 DE Anti-prion peptide inhibiting abnormal protein folding.  
 XX Anti-amyloid peptide; IAbeta; abnormal protein folding inhibitor;  
 KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;  
 KW human prion disease; Kuru; Creutzfeldt-Jakob disease;  
 KW Gerstmann-Strausler-Scheinker Syndrome; animal prion disease;  
 KW prion associated human neurodegenerative disease; scrapie;  
 KW spongiform encephalopathy; transmissible mink encephalopathy;  
 KW chronic wasting disease; mule; deer; elk; human.  
 XX Homo sapiens.  
 OS Synthetic.  
 OS WO9639834-A1.  
 PN 19-DEC-1996.  
 PD 06-JUN-1996; 96WO-US10220.  
 PF 10-APR-1996; 96US-0630645.  
 PR 07-JUN-1995; 95US-0478326.  
 XX (UYN ) UNIV NEW YORK STATE.  
 PA Baumann MH, Frangione B, Soto-Jara C;  
 PI WPI; 1997-051637/05.  
 DR New inhibitors of fibrillogenesis proteins or peptides - used for  
 XX preventing, treating or detecting amyloidosis disorders such as  
 PT Alzheimer's disease.  
 PT Claim 15; Page 40; 63pp: English.  
 PS A method has been developed for the prevention or treatment of a  
 XX disorder or disease associated with the formation of amyloid or  
 CC amyloid-like deposits, involving the formation of a protein  
 CC or peptide. The method involves administering an inhibitory peptide  
 CC which prevents the abnormal folding or which dissolves existing amyloid  
 CC or amyloid-like deposits, where the peptide comprises a sequence of  
 CC 3-15 amino acid residues and has a hydrophobic cluster of at least 3  
 CC amino acids, where at least one of the 3 amino acids is a beta-sheet  
 CC blocking amino acid residue selected from Pro, Gly, Asn and His. The  
 CC present sequence represents a specifically claimed example of an anti-  
 CC prion peptide which inhibits abnormal protein folding. The inhibitory  
 CC peptide is capable of associating with a structural determinant on the  
 CC protein or peptide to structurally block and inhibit the abnormal  
 CC folding into amyloid or amyloid-like deposits. The method can be used  
 CC for preventing, treating or detecting e.g. Alzheimer's dementia or  
 CC diseases. Down's syndrome, other amyloidosis disorders, human prion  
 CC diseases such as Kuru, Creutzfeldt-Jakob disease, Gerstmann-Strausler-  
 CC Scheinker Syndrome, prion associated human neurodegenerative diseases or  
 CC animal prion diseases such as scrapie, spongiform encephalopathy,  
 CC transmissible mink encephalopathy and chronic wasting disease of mule  
 CC deer and elk.  
 CC

SQ Sequence 7 AA:

Query Match 22.7%: Score 5; DB 18; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPV 13  
| | | | |  
DB 1 aapv 5

RESULT 7

AAB37838  
ID AAB37838 standard; Peptide: 8 AA.

AC AAB37838;

DT 26-FEB-2001 (first entry)

DE Neisserial conserved peptide #21.

KW Neisseria meningitidis; Neisseria gonorrhoeae; antibacterial;

KM gene therapy; conserved sequence.

OS Neisseria sp.

PN WO20006741-A2.

PD 09-NOV-2000.

PE 28-APR-2000; 2000WO-1B00642.

PR 30-APR-1999; 99GB-0010168.

PR 09-MAR-2000; 2000GB-0005728.

PA (CHIR-) CHIRON SPA.

PI Rappunli R;

DR WPI; 2000-687543/67.

XX Novel Neisserial protein fragments and their corresponding nucleic  
PT acids, useful in the manufacture of medicines for the prevention of  
PT Neisserial infection, and in the manufacture of diagnostic reagents -

PS Claim 15; Page 57; 157pp; English.

CC The present peptide is a conserved region of a Neisserial protein.

CC Neisserial proteins containing this sequence, and the nucleic acids  
CC that encode such proteins, are useful in the manufacture of medicines  
CC for the prevention of Neisserial infection, and in the manufacture of  
CC multi-specific diagnostic reagents.

SQ Sequence 8 AA:

Query Match 22.7%: Score 5; DB 21; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPV 13  
| | | | |  
DB 4 aapv 8

RESULT 8

ID AAM44355 standard; peptide: 9 AA.

AC AAM44355;

DT 28-MAY-1998 (first entry)

XX Breast cancer-associated protein fragment BC-2 SEQ ID NO:3.  
DE  
XX

KW Human: breast cancer-associated protein; nuclear matrix protein;  
KM detection; diagnosis; antibody.

OS Homo sapiens.

PN WO9746884-A1.

PD 11-DEC-1997.

PF 03-JUN-1997; 97WO-US09529.

PR 05-JUN-1996; 96US-0658639.

PA (MATR-) MATRITTECH INC.

PI Keesee SK, Obar R, Wu Y;

DR WPI; 1998-042336/04.

XX Diagnosing breast cancer by detecting a breast cancer-associated  
PT protein - allows early and reliable diagnosis and treatment  
PT monitoring, and antibody or inhibitory compounds useful for treating  
PT breast cancer

PS Claim 6; Page 29; 47pp; English.

XX The present sequence represents a breast cancer-associated protein  
CC fragment for use in a method for diagnosing breast cancer in tissue  
CC or body fluid by detecting one or more breast cancer-associated  
CC protein(s). Alternatively a nucleic acid encoding a breast cancer-  
CC associated protein is detected in the sample by the use of a nucleic  
CC acid probe. The breast cancer-associated proteins, encoding nucleic  
CC acids and antibodies are useful in diagnostic assays and kits for  
CC breast cancer detection. The proteins are also useful in screening for  
CC antibody compounds and monitoring effectiveness of treatments. The  
CC antibody, or pharmaceutical compositions containing the antibody or  
CC the inhibitory compound, can be administered to patients to treat  
CC breast cancer. The methods allow reliable and early diagnosis of  
CC breast cancer, or prediction of its onset, by detection of specific  
CC markers expressed in breast tumour cells but not in non-cancerous  
CC breast cells.

SQ Sequence 9 AA:

Query Match 22.7%: Score 5; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEAHA 10  
| | | | |  
DB 2 aaaaa 6

RESULT 9

AAR96835  
ID AAR96835 standard; peptide: 11 AA.

AC AAR96835;

DT 29-NOV-1996 (first entry)

XX Human neurofilament triplet h fragment, homologous to Neisseria Iga-  
DE alpha1.  
XX

KW Iga protease precursor; Ipp; bacterial polypeptide; autoimmune;

KM viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;

KW human neurofilament triplet h protein; Nfn; Neisseria gonorrhoeae;  
MS11.  
XX

```

OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 1..3
FT /note= "identical to sequence in Neisseria gonorrhoeae
FT Iga-alpha1"
FT Region 5..7
FT /note= "identical to sequence in Neisseria gonorrhoeae
FT Iga-alpha1"
FT Region 10..11
FT /note= "identical to sequence in Neisseria gonorrhoeae
FT Iga-alpha1"
XX
XX MO9609395-A2.
XX
XX 28-MAR-1996.
XX
XX 21-SEP-1995; 95WO-EP03726.
XX
XX 21-SEP-1994; 94DE-4433708.
XX
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Beck SC, Jose J, Lorenzen DR, Meyer TFF, Oetzelberger KB;
XX Pohlner J, Woelk U;
XX WPI: 1996-188456/19.
XX
XX Medicaments for treating auto-immune or viral diseases - contg.
XX PT substances interfering with bacterial poly:protein function
XX
XX Claim 32; Fig 2; 117pp; German.
XX
XX
XX The present sequence from human neurofilament triplet h protein has
XX homology to a cleavage product from the Iga-alpha1 domain of the
XX precursor of Iga-protease polypeptide (IPP) of Neisseria gonorrhoeae
XX strain MS11. The Neisseria IPP has been implicated in rheumatoid
XX arthritis and other auto-immune diseases. The polypeptide also
XX activates proviruses, including HIV. Substances which interfere with
XX the function of IPP from Neisseria will be useful for treating
XX associated autoimmune diseases and viral infections. Peptides
XX comprising the homology region sequences, whether from Neisseria or
XX from humans, are claimed.
XX
XX Sequence 11 AA:
XX
XX
XX Query Match 22.7%; Score 5; DB 17; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 91;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 6 AAAAA 10
XX |
XX |
XX |
XX |
XX |
XX 7 aaaaa 11
XX
XX
XX RESULT 10
XX AAR51235
XX ID AAR51235 standard; Protein; 12 AA.
XX
XX AAR51235;
XX
XX 25-OCT-1994 (first entry)
XX
XX Part of pNIPenV including a functional B1.8scFv antibody.
XX
XX Moloney murine leukaemia virus; B1.8scFv antibody;
XX B1.8scFv antibody.
XX
XX Chimeric Moloney murine leukaemia virus.
XX Chimeric Mus musculus.
XX
XX Key Location/Qualifiers

```

```

FT Peptide 1..7
FT /label= part of B1.8scFv antibody
XX
XX MO9406920-A.
XX
XX 31-MAR-1994.
XX
XX 22-SEP-1993; 93WO-GB01992.
XX
XX 22-SEP-1992; 92GB-0020010.
XX 11-MAR-1993; 93GB-0004962.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Hawkins RE, Russell SJ, Winter GP;
XX WPI: 1994-118469/14.
XX DR N-PSDB; AAQ45194.
XX
XX Recombinant virus particles displaying nonviral polypeptide on
XX the surface - able to infect eukaryotic cells, useful for
XX targeted gene therapy, e.g. of tumours
XX
XX Example 1; Page 64; 78pp; English.
XX
XX AAR51235 shows the second part of the amino acid sequence of the
XX B1.8-env fusion protein generated in pNIPenV. The first part
XX of the sequence is shown in AAR51234. Recombinant retroviruses
XX expressed a functional surface B1.8 single chain Ab.
XX Ab fragments on the surface of recombinant retroviral particles
XX could be used to target virus to cells for gene delivery, or to
XX retain the virus in target tissues, or for the construction of
XX libraries of viral display packages.
XX
XX Sequence 12 AA:
XX
XX
XX Query Match 22.7%; Score 5; DB 15; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 98;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 7 EAAAP 11
XX |
XX |
XX |
XX |
XX |
XX 4 eaap 8
XX
XX
XX RESULT 11
XX AAW32549
XX ID AAW32549 standard; peptide; 12 AA.
XX
XX AAW32549;
XX
XX 21-JAN-1998 (first entry)
XX
XX Anti-prion peptide inhibiting abnormal protein folding.
XX
XX Anti-amyloid peptide; Iabeta; abnormal protein folding inhibitor;
XX Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;
XX human prion disease; Kuru; Creutzfeldt-Jakob disease;
XX Gerstmann-Strausler-Scheinker Syndrome; animal prion disease;
XX prion associated human neurodegenerative disease; scrapie;
XX spongiform encephalopathy; transmissible mink encephalopathy;
XX chronic wasting disease; mule; deer; elk; human.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX MO9639834-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US10220.
XX

```

```

PR 10-APR-1996; 96US-0630645.
PR 07-JUN-1995; 95US-0478326.
XX
PA (UNYNY ) UNIV NEW YORK STATE.
XX
PI Baumann MH, Frangione B, Soto-Jara C;
XX
DR WPI: 1997-051637/05.
XX
PT New inhibitors of fibrillogenesis proteins or peptides - used for
PT preventing, treating or detecting amyloidosis disorders such as
PT Alzheimer's disease.
XX
PS
XX Claim 15; Page 40; 63pp; English.
XX
CC A method has been developed for the prevention or treatment of a
CC disorder or disease associated with the formation of amyloid or
CC amyloid-like deposits, involving the abnormal folding of a protein
CC or peptide. The method involves administering an inhibitory peptide
CC which prevents the abnormal folding or which dissolves existing amyloid
CC or amyloid-like deposits, where the peptide comprises a sequence of
CC 3-15 amino acid residues and has a hydrophobic cluster of at least 3
CC amino acids, where at least one of the 3 amino acids is a beta-sheet
CC blocking amino acid residue selected from Pro, Gly, Asn and His. The
CC present sequence represents a specifically claimed example of an anti-
CC prion peptide which inhibits abnormal protein folding. The inhibitory
CC peptide is capable of associating with a structural determinant on the
CC protein or peptide to structurally block and inhibit the abnormal
CC folding into amyloid or amyloid-like deposits. The method can be used
CC for preventing, treating or detecting e.g. Alzheimer's dementia or
CC disease, Down's syndrome, other amyloidosis disorders, human prion
CC diseases such as Kuru, Creutzfeldt-Jakob disease, Gerstmann-Strausler-
CC Scheinker Syndrome, prion associated human neurodegenerative diseases or
CC animal prion diseases such as scrapie, spongiform encephalopathy,
CC transmissible mink encephalopathy and chronic wasting disease of mule
CC deer and elk.
XX
SQ Sequence 12 AA:

Query Match 22.7%; Score 5; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AAPVY 13
   | | | | |
Db 5 aapvv 9

RESULT 12
AAW38350
ID AAW38350 standard; Peptide: 13 AA.
XX
AC AAW38350;
XX
DT 08-JUN-1998 (first entry)
XX
DE Apoptosis associated protein Bdk BH3 domain mutant PW-LVLEE.
XX
KW Apoptosis associated protein; Bdk; BH3 domain; human; cell death;
KW cell proliferation; degenerative disorder; gene therapy;
KW Alzheimer's disease; autoimmune disease; cancer; inflammation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN MO9745128-A1.
XX
PD 04-DEC-1997.
XX
PF 29-MAY-1997; 97WO-US09194.
XX
PR 29-MAY-1996; 96US-0632514.

```

```

XX
PA (APOP-) APOPTOSIS TECHNOLOGY INC.
XX
PI Gallo GJ;
XX
DR WPI: 1998-032326/03.
XX
PT Human apoptosis associated protein Bdk - useful to treat
PT degenerative disorders characterised by inappropriate cell death or
PT proliferation
XX
PS
XX Example 8; Fig 9B; 110pp; English.
XX
CC This peptide comprises alanine scanning mutant PW-LVLEE of the BH3
CC domain (see AAW38346) of human Bdk (see AAW38358), a novel apoptosis
CC associated protein that can induce apoptosis in cells. PW-LVLEE
CC contains 5 alanine substitutions in the BH3 element. It has
CC completely lost BH3's apoptosis induction capabilities, supporting
CC the conclusion that the BH3 region is absolutely necessary for
CC Bdk's apoptotic function. Bdk and its BH3 domain can be used to
CC treat degenerative disorders characterised by inappropriate cell
CC death or proliferation.
XX
SQ Sequence 13 AA:

Query Match 22.7%; Score 5; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAAA 10
   | | | | |
Db 8 aaaaa 12

RESULT 13
AA82047
ID AAW82047 standard; peptide: 15 AA.
XX
AC AAW82047;
XX
DT 01-JUN-2000 (first entry)
XX
DE MHC class II protein binding peptide SPQ ID NO:15.
XX
KW MHC class II; major histocompatibility complex; autoimmune disease;
KW inflammatory disease; binding; rheumatoid arthritis; antiinflammatory;
KW antiarthritic; multiple sclerosis.
XX
OS Synthetic.
XX
PN WO200005249-A2.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16617.
XX
PR 23-JUL-1998; 98US-0093859.
PR 09-MAR-1999; 99US-0123675.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Harell M;
XX
DR WPI: 2000-205374/18.
XX
PT New synthetic peptide, useful for treating autoimmune disease, e.g.
PT rheumatoid arthritis -
XX
PS Claim 22; Page 40; 57pp; English.
XX
CC The present invention describes synthetic peptides having an amino acid
CC sequence comprising at least 3 residues selected from the group of amino

```

CC acids consisting of aromatic acids, negatively charged amino acids,  
CC positively charged amino acids, and aliphatic amino acids, the synthetic  
CC peptides being at least 7 amino acid residues in length and capable of  
CC binding to a major histocompatibility complex (MHC) class II protein  
CC associated with an autoimmune disease. The synthetic peptides have  
CC anti-inflammatory and anti-arthritis activities. They are used to treat  
CC inflammatory and demyelinating autoimmune diseases, especially  
CC rheumatoid arthritis and multiple sclerosis. The peptides are specific  
CC for particular MHC Class II alleles. Purified, short and synthetic  
CC peptides should have fewer side effects than mixtures of random  
CC peptides; may include many repeats of the active sequence and/or contain  
CC amino acid analogues that improve stability (or other desired features).  
CC AAY82021 to AAY82044 represent specifically claimed peptide sequences  
CC which can be used as part of the synthetic peptides of the present  
CC invention; AAY82045 to AAY82063 represent specifically claimed examples  
CC of the synthetic peptides from the present invention; and AAY82064 to  
CC AAY82080 represent other peptides used in the exemplification of the  
CC present invention.

Query Match 22.7%; Score 5; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAAA 10  
|1111  
Db 5 aaaaa 9

## RESULT 14

AAY82059  
ID AAY82059 standard; peptide: 15 AA.

AC AAY82059;

DT 01-JUN-2000 (first entry)

DE MHC class II protein binding peptide SEQ ID NO:29.

XX MHC class II; major histocompatibility complex; autoimmune disease;

KW inflammatory disease; binding; rheumatoid arthritis; antinflammatory;

KM antiarthritic; multiple sclerosis.

OS Synthetic.

PN WO200005249-A2.

PD 03-FEB-2000.

PF 22-JUL-1999; 99WO-US16617.

PR 23-JUL-1998; 98US-0093859.

PR 09-MAR-1999; 99US-0123675.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Harell M;

DR WPI: 2000-205374/18.

XX New synthetic peptide, useful for treating autoimmune disease, e.g.

PT rheumatoid arthritis -

PS Claim 24; Page 41; 57pp; English.

XX The present invention describes synthetic peptides having an amino acid  
CC sequence comprising at least 3 residues selected from the group of amino  
CC acids consisting of aromatic acids, negatively charged amino acids,  
CC positively charged amino acids, and aliphatic amino acids, the synthetic  
CC peptides being at least 7 amino acid residues in length and capable of  
CC binding to a major histocompatibility complex (MHC) class II protein

CC associated with an autoimmune disease. The synthetic peptides have  
CC anti-inflammatory and anti-arthritis activities. They are used to treat  
CC inflammatory and demyelinating autoimmune diseases, especially  
CC rheumatoid arthritis and multiple sclerosis. The peptides are specific  
CC for particular MHC Class II alleles. Purified, short and synthetic  
CC peptides should have fewer side effects than mixtures of random  
CC peptides; may include many repeats of the active sequence and/or contain  
CC amino acid analogues that improve stability (or other desired features).  
CC AAY82021 to AAY82044 represent specifically claimed peptide sequences  
CC which can be used as part of the synthetic peptides of the present  
CC invention; AAY82045 to AAY82063 represent specifically claimed examples  
CC of the synthetic peptides from the present invention; and AAY82064 to  
CC AAY82080 represent other peptides used in the exemplification of the  
CC present invention.

Query Match 22.7%; Score 5; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAAA 10  
|1111  
Db 5 aaaaa 9

## RESULT 15

AAY82062  
ID AAY82062 standard; peptide: 15 AA.

AC AAY82062;

DT 01-JUN-2000 (first entry)

DE MHC class II protein binding peptide SEQ ID NO:35.

XX MHC class II; major histocompatibility complex; autoimmune disease;

KW inflammatory disease; binding; rheumatoid arthritis; antinflammatory;

KM antiarthritic; multiple sclerosis.

OS Synthetic.

PN WO200005249-A2.

PD 03-FEB-2000.

PF 22-JUL-1999; 99WO-US16617.

PR 23-JUL-1998; 98US-0093859.

PR 09-MAR-1999; 99US-0123675.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Harell M;

DR WPI: 2000-205374/18.

XX New synthetic peptide, useful for treating autoimmune disease, e.g.

PT rheumatoid arthritis -

PS Claim 24; Page 41; 57pp; English.

XX The present invention describes synthetic peptides having an amino acid  
CC sequence comprising at least 3 residues selected from the group of amino  
CC acids consisting of aromatic acids, negatively charged amino acids,  
CC positively charged amino acids, and aliphatic amino acids, the synthetic  
CC peptides being at least 7 amino acid residues in length and capable of  
CC binding to a major histocompatibility complex (MHC) class II protein  
CC associated with an autoimmune disease. The synthetic peptides have  
CC anti-inflammatory and anti-arthritis activities. They are used to treat  
CC inflammatory and demyelinating autoimmune diseases, especially  
CC rheumatoid arthritis and multiple sclerosis. The peptides are specific

CC for particular MHC Class II alleles. Purified, short and synthetic  
CC peptides should have fewer side effects than mixtures of random  
CC peptides; may include many repeats of the active sequence and/or contain  
CC amino acid analogues that improve stability (or other desired features).  
CC AA182021 to AA182044 represent specifically claimed peptide sequences  
CC which can be used as part of the synthetic peptides of the present  
CC invention; AA182045 to AA182063 represent specifically claimed examples  
CC of the synthetic peptides from the present invention; and AA182064 to  
CC AA182080 represent other peptides used in the exemplification of the  
CC present invention.

XX  
SQ Sequence 15 AA:

Query Match 22.7%; Score 5; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAAA 10  
|||  
Db 4 aaaaa 8

Search completed: July 23, 2001, 16:56:13  
Job time: 530 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: July 23, 2001, 17:06:06 ; Search time 69.82 Seconds  
(without alignments)  
41.689 Million cell updates/sec

Title: US-09-351-296-15

Perfect score: 22

Sequence: 1 QATROADIDQPAIQSSWPKLEQ 22

Scoring table: OLIGO

Searched: 425026 seqs, 132305027 residues

Word size: 0

Total number of hits satisfying chosen parameters: 5654

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database:

SPTREMBL\_16:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.unclassified:\*  
13: sp.vertebrate:\*  
14: sp.virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	18.2	16	4 09UD41	09UD41 homo sapien
2	4	18.2	21	14 093044	093044 maize strea
3	4	18.2	21	14 093046	093046 maize strea
4	4	18.2	21	14 093047	093047 maize strea
5	4	18.2	22	10 09SA04	09SA04 arabidopsis
6	4	18.2	22	11 09QUY0	09QUY0 ratu sp.
7	4	18.2	22	11 09QUX9	09QUX9 ratu sp.
8	3	13.6	8	5 015886	015886 babesia bov
9	3	13.6	8	5 P82686	P82686 periplaneta
10	3	13.6	8	5 P82688	P82688 periplaneta
11	3	13.6	9	4 P70740	P70740 alcaligenes
12	3	13.6	9	4 016605	016605 homo sapien
13	3	13.6	9	11 09QMG2	09QMG2 mus musculu
14	3	13.6	9	14 090350	090350 hepatitis g
15	3	13.6	10	4 09UCS3	09UCS3 homo sapien
16	3	13.6	10	14 066190	066190 avian infec
17	3	13.6	11	2 09RF22	09RF22 mycoplasma
18	3	13.6	11	5 09NFX0	09NFX0 drosophila
19	3	13.6	11	11 062207	062207 mus musculu

20	3	13.6	12	2 09X6X0	09X6X0 aquifex pyr
21	3	13.6	12	2 052112	052112 acinetobact
22	3	13.6	12	14 085631	085631 avian retro
23	3	13.6	13	2 047601	047601 escherichia
24	3	13.6	13	2 055094	055094 synechocyst
25	3	13.6	13	4 09Y674	09Y674 homo sapien
26	3	13.6	13	5 024365	024365 drosophila
27	3	13.6	13	8 09X1R2	09X1R2 hemisia tab
28	3	13.6	13	8 09T569	09T569 zea mays (m
29	3	13.6	14	10 09F0X5	09F0X5 symphoricar
30	3	13.6	15	2 046456	046456 clostridium
31	3	13.6	15	2 054325	054325 staphylococ
32	3	13.6	15	2 005991	005991 staphylococ
33	3	13.6	15	2 09R598	09R598 micrococcu
34	3	13.6	15	4 09UCR3	09UCR3 homo sapien
35	3	13.6	15	5 027201	027201 tetrahymena
36	3	13.6	15	5 097430	097430 drosophila
37	3	13.6	15	6 09TR54	09TR54 ovis aries
38	3	13.6	15	11 09QV76	09QV76 mus sp. pre
39	3	13.6	15	11 09QV17	09QV17 ratu sp.
40	3	13.6	15	14 085713	085713 rous sarcom
41	3	13.6	16	2 045260	045260 bradyrhizob
42	3	13.6	16	2 09R425	09R425 streptococc
43	3	13.6	16	2 09KHM6	09KHM6 synechococc
44	3	13.6	16	5 09TWC5	09TWC5 dirofilaria
45	3	13.6	16	6 09TRR1	09TRR1 oryctolagus

## ALIGNMENTS

RESULT 1  
ID 09UD41 PRELIMINARY; PRT; 16 AA.  
AC 09UD41;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE BETA-TSOFORF THYROID HORMONE RECEPTOR (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95105146; Pubmed=7528740;  
RA Flynn T.R., Hollenberg A.N., Cohen O., Menke J.B., Usala S.J.,  
RA Tollin S., Hegarty M.K., Mondisford F.E.;  
RT "A novel C-terminal domain in the thyroid hormone receptor selectively  
mediates thyroid hormone inhibition."  
RT J. Biol. Chem. 269:32713-32716(1994).  
RL  
SQ SEQUENCE 16 AA; 1920 MW; 79A831A4F3C8E22F CRC64;

Query Match 18.28; Score 4; DB 4; Length 16;  
Best Local Similarity 100.08; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 17 WPKL 20  
DB 2 WPKL 5  
RESULT 2  
ID 093044 PRELIMINARY; PRT; 21 AA.  
AC 093044;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE 17.6 KDA REPB PROTEIN (FRAGMENT).  
GN REPB.  
OS Maize streak virus.

OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.  
OX NCBI\_TaxID=10821;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SP1 FROM REUNION ISLAND;  
RX MEDLINE=97049057; PubMed=8893787;  
RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;  
RT "Infectivity and complete nucleotide sequence of the genome of a  
RT genetically distinct strain of maize streak virus from Reunion  
RT Island.";  
RL Arch. Virol. 141:1637-1650(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SP1 FROM REUNION ISLAND;  
RA Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;  
RT "Quasispecies nature of three related maize streak virus isolates  
RT obtained through different mode of selection.";  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ224999; CAA12284.1; -  
FT NON\_TER 21 21  
SQ SEQUENCE 21 AA; 2364 MW; 267B619FB84E782B CRC64;

Query Match 18.2%; Score 4; DB 14; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 IQSS 16  
||||  
DB 6 IQSS 9

RESULT 3  
093046 PRELIMINARY; PRT; 21 AA.  
AC 093046;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE 17.6 KDA REPB PROTEIN (FRAGMENT).  
GN REPB.  
OS Maize streak virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.  
OX NCBI\_TaxID=10821;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SP1 FROM REUNION ISLAND;  
RX MEDLINE=97049057; PubMed=8893787;  
RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;  
RT "Infectivity and complete nucleotide sequence of the genome of a  
RT genetically distinct strain of maize streak virus from Reunion  
RT Island.";  
RL Arch. Virol. 141:1637-1650(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SP1 FROM REUNION ISLAND;  
RA Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;  
RT "Quasispecies nature of three related maize streak virus isolates  
RT obtained through different mode of selection.";  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ225000; CAA12287.1; -  
FT NON\_TER 21 21  
SQ SEQUENCE 21 AA; 2364 MW; 267B619FB84E782B CRC64;

Query Match 18.2%; Score 4; DB 14; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 IQSS 16  
||||  
DB 6 IQSS 9

RESULT 4  
093047 PRELIMINARY; PRT; 21 AA.  
AC 093047;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE 17.6 KDA REPB PROTEIN (FRAGMENT).  
GN REPB.  
OS Maize streak virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.  
OX NCBI\_TaxID=10821;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SP1 FROM REUNION ISLAND;  
RX MEDLINE=97049057; PubMed=8893787;  
RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;  
RT "Infectivity and complete nucleotide sequence of the genome of a  
RT genetically distinct strain of maize streak virus from Reunion  
RT Island.";  
RL Arch. Virol. 141:1637-1650(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SP1 FROM REUNION ISLAND;  
RA Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;  
RT "Quasispecies nature of three related maize streak virus isolates  
RT obtained through different mode of selection.";  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ225001; CAA12290.1; -  
FT NON\_TER 21 21  
SQ SEQUENCE 21 AA; 2364 MW; 267B619FB84E782B CRC64;

Query Match 18.2%; Score 4; DB 14; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 IQSS 16  
||||  
DB 6 IQSS 9

RESULT 5  
09SAU4 PRELIMINARY; PRT; 22 AA.  
AC 09SAU4;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE CHALCONE SYNTHASE (FRAGMENT).  
GN CHS.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CV. COLUMBIA;  
RX MEDLINE=93144713; PubMed=8425063;  
RA Trezlini G.F., Horlicks A., Somsich I.E.;  
RT "Isolation of putative defense-related genes from Arabidopsis thaliana  
RT and expression in fungal elicitor-treated cells.";  
RL Plant Mol. Biol. 21:385-389(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CV. COLUMBIA;  
RX MEDLINE=98187255; PubMed=9526507;  
RA Hartmann U., Valentine W.J., Christie J.M., Hays J., Jenkins G.I.,  
RA Weisshaar B.;  
RT "Identification of UV/blue light-response elements in the Arabidopsis  
RT thaliana chalcone synthase promoter using a homologous protoplast



RT transient expression system."  
 RL Plant Mol. Biol. 36:741-754(1998).  
 DR EMBL: AF012810; AAC17466.1; -.  
 FT NON\_TER 22  
 SQ SEQUENCE 22 AA; 2275 MW; 0D31732B4630BD74 CRC64;

Query Match 18.2%; Score 4; DB 10; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 6e+02; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

Qy 4 ROAQ 7  
 ||||  
 Db 13 RQAO 16

RESULT 6  
 ID 09OUY0 PRELIMINARY; PRT; 22 AA.  
 AC 09OUY0;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE FOLATE BINDING PROTEIN I (FRAGMENT).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96139323; Pubmed=8547345;  
 RA da Costa M., Rothenberg S.P.;  
 RT "Purification and characterization of folate binding proteins from rat placenta."  
 RL Biochim. Biophys. Acta 1292:23-30(1996).  
 SQ SEQUENCE 22 AA; 2566 MW; FE8BD422D86E5EFB CRC64;

Query Match 18.2%; Score 4; DB 11; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 6e+02; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 QATR 4  
 ||||  
 Db 1 QATR 4

RESULT 7  
 ID 09OUX9 PRELIMINARY; PRT; 22 AA.  
 AC 09OUX9;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE FOLATE BINDING PROTEIN II (FRAGMENT).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96139323; Pubmed=8547345;  
 RA da Costa M., Rothenberg S.P.;  
 RT "Purification and characterization of folate binding proteins from rat placenta."  
 RL Biochim. Biophys. Acta 1292:23-30(1996).  
 SQ SEQUENCE 22 AA; 2543 MW; E91E70283D8CD4FB CRC64;

Query Match 18.2%; Score 4; DB 11; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 6e+02; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 QATR 4  
 ||||  
 Db 1 QATR 4

RESULT 8  
 ID 015896 PRELIMINARY; PRT; 8 AA.  
 AC 015896;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DE 12D3 ANTIGEN (FRAGMENT).  
 GN 12D3.  
 OS Babesia bovis.  
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.  
 OX NCBI\_TaxID=5865;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPRAIN-SAMFORD;  
 RA Sillins G.U., Blakeley R.L., Riddles P.W.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U44917; AAB66362.1; -.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 984 MW; F0D2C9D411ADD726 CRC64;

Query Match 13.6%; Score 3; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+05; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0;

Qy 2 ATR 4  
 ||||  
 Db 3 ATR 5

RESULT 9  
 ID P82686 PRELIMINARY; PRT; 8 AA.  
 AC P82686;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE KININ-2 (PEA-K-2).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta;  
 OC Pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Blattoidea; Blattellidae; Dictyoptera; Blattaria;  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE AND FUNCTION.  
 RC TISSUE=CORPORA CARDIACA;  
 RX MEDLINE=98010462; Pubmed=9350979;  
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana."  
 RL Regul. Pept. 71:199-205(1997).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8  
 SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BD4 CRC64;

Query Match 13.6%; Score 3; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+05; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0;

Qy 15 SSW 17  
 ||||  
 Db 5 SSW 7

```

RESULT 10
P82688 ID PRELIMINARY: PRT: 8 AA.
AC P82688;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattellidae; Periplaneta.
OX NCBI_Taxid=6978;
RN [1]
RP SEQUENCE AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC Neuropeptide; Amidation.
KM MOD.RES 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;

```

```

Query Match 13.6%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 15 SSW 17
DB 5 SSW 7

```

```

RESULT 11
P70740 ID PRELIMINARY: PRT: 9 AA.
AC P70740;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HOXA, HOXA AND HYPE GENES (FRAGMENT).
GN HOXA.
OS Alcaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_Taxid=510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H16;
RX MEDLINE=94292469; PubMed=8021224;
RA Lenz O., Schwartz E., Dornedde J., Eitinger M., Friedrich B.;
RT "The Alcaligenes eutrophus H16 hoxx gene participates in hydrogenase
RT regulation.";
RL J. Bacteriol. 176:4385-4393(1994).
DR EMBL; X74670; CAA52736.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 992 MW; 970BD1ADC6D33AB5 CRC64;

```

```

Query Match 13.6%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 OAT 3
DB 1

```

```

DB 5 OAT 7
RESULT 12
O16605 ID PRELIMINARY: PRT: 9 AA.
AC O16605;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-NOV-1996 (TREMBlrel. 08, Last annotation update)
DE GLUTATHIONE S-TRANSFERASE 2 (FRAGMENT).
GN GSTA2 OR GSTT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88330756; PubMed=3138230;
RA Chow N.W., Whang-Peng J., Kao-Shan C.S., Tam M.F., Lai H.C., Tu C.P.;
RT "Human glutathione S-transferases. The Ha multigene family encodes
RT products of different but overlapping substrate specificities.";
RL J. Biol. Chem. 263:12797-12800(1988).
DR EMBL; M21867; AAA52617.1; -.
DR EMBL; M21866; AAA35938.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1116 MW; D168E72327633BID CRC64;

```

```

Query Match 13.6%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 18 PKL 20
DB 5 PKL 7

```

```

RESULT 13
O90WG2 ID PRELIMINARY: PRT: 9 AA.
AC O90WG2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PROTEIN G BETA-2 SUBUNIT (FRAGMENT).
GN GNB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98030528; PubMed=9365246;
RA Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
RA Lacombe C.;
RT "Abnormal erythropoietin (Epo) gene expression in the murine
RT erythroleukemia IM32 cells is issued from a rearrangement between the
RT G-protein b2 gene subunit and the Epo genes.";
RL Oncogene 15:1995-1999(1997).
DR EMBL; Y11970; CAA72706.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1133 MW; 86FD0736DB172B05 CRC64;

```

```

Query Match 13.6%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 20 LEQ 22
DB 4 LEQ 6

```

## RESULT 14

090350  
ID 090350 PRELIMINARY; PRT; 9 AA.  
AC 090350;  
DT 01-NOV-1998 (TReMBLrel. 08, Created)  
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE POLYPROTEIN (FRAGMENT).  
OS Hepatitis G virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC GBV-C/HGV group.  
NCBI\_TaxID=45255;  
OX [1]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=SG3419;  
RA Wong J., Chan S.H., Ren E.C.;  
RT "HGV Isolates from Singapore: Evidence for novel Asian variants."  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF078065; AAC32371.1; -  
KW Polypeptide.  
FT NON\_PEP  
SQ SEQUENCE 9 AA: 989 MW: D95CA5A5EB9BCDD CRC64;

## Query Match

Best Local Similarity 13.6%; Score 3; DB 14; Length 9;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 SSW 17  
|||

Db 7 SSW 9

## RESULT 15

09UCS3  
ID 09UCS3 PRELIMINARY; PRT; 10 AA.  
AC 09UCS3;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
DE TROPOMYOSIN=3 KDA CALCIUM BINDING PROTEIN FRAGMENT D.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP  
RP SEQUENCE.  
RX MEDLINE=92090441; PubMed=1836432;  
RA Crabos M., Yamakado T., Heizmann C.W., Cerletti N., Buhler F.R.,  
RA Erne P.;  
RT "The calcium binding protein tropomyosin in human platelets and  
cardiac tissue: elevation in hypertensive cardiac hypertrophy."  
RL Eur. J. Clin. Invest. 21:472-478(1991).  
SQ SEQUENCE 10 AA: 1126 MW: 7A4FD3DC2DAFAEB CRC64;

## Query Match

Best Local Similarity 13.6%; Score 3; DB 4; Length 10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 KLE 21  
|||

Db 8 KLE 10

Search completed: July 23, 2001, 17:06:07  
Job time: 548 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: July 23, 2001, 17:04:50 ; Search time 23.18 Seconds  
(Without alignments)  
32.512 Million cell updates/sec

Title: US-09-351-296-15

Perfect score: 22

Sequence: 1 QATROAQDIPAIQSSWPKLEQ 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1176

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	18.2	13	1	ACT7_SOYBN
2	4	18.2	17	1	ACT6_SOYBN
3	3	13.6	6	1	LOK1_LOCM1
4	3	13.6	7	1	LANC_CARUI
5	3	13.6	8	1	LCK2_LEUMA
6	3	13.6	8	1	LCK3_LEUMA
7	3	13.6	8	1	LCK6_LEUMA
8	3	13.6	8	1	LCK7_LEUMA
9	3	13.6	9	1	OXYT_BURE
10	3	13.6	9	1	ULAH_HUMAN
11	3	13.6	10	1	PNEU_HUMAN
12	3	13.6	10	1	PNEU_RAT
13	3	13.6	12	1	TM2A_METMA
14	3	13.6	13	1	CRTC_BOVIN
15	3	13.6	13	1	HPAL_RANES
16	3	13.6	13	1	UVRD_SAFETY
17	3	13.6	14	1	ATP6_SPTOL
18	3	13.6	15	1	FGF1_CANFA
19	3	13.6	15	1	LECI_PSOCA
20	3	13.6	15	1	UC30_MAIZE
21	3	13.6	17	1	JHBP_PLAVG
22	3	13.6	17	1	UNIS_CLOPA
23	3	13.6	18	1	LUXB_KRTAS
24	3	13.6	18	1	PSAI_SPTOL
25	3	13.6	20	1	A1BG_EQUAS
26	3	13.6	20	1	COG1_PACRM
27	3	13.6	20	1	COXB_THROB
28	3	13.6	20	1	COXB_ONCMY
29	3	13.6	20	1	DER6_DERPT
30	3	13.6	20	1	ELAS_GADMO
31	3	13.6	20	1	HELT_HELHO
32	3	13.6	20	1	M17_BOVIN
33	3	13.6	21	1	FIBB_BUBBU

34	3	13.6	21	1	PSAL_SYNP6	P31084 synechococ
35	3	13.6	21	1	SRTD_ATREN	P13211 attractaspis
36	3	13.6	22	1	MOTI_CHICK	O09066 gallus gall
37	2	9.1	6	1	ACPH_RABIT	P25154 oryctolagus
38	2	9.1	7	1	CIA_ENTFA	P11932 entlerococcu
39	2	9.1	7	1	UF04_MOUSE	P38642 mus musculu
40	2	9.1	7	1	UH11_RAT	P56576 rattus norv
41	2	9.1	8	1	ACT_CARMA	P80709 carcius ma
42	2	9.1	8	1	AKH_CITBAU	P25418 libellula a
43	2	9.1	8	1	CLP_THICU	P80488 thiodacillu
44	2	9.1	8	1	LCK1_LEUMA	P21140 leucophaea
45	2	9.1	8	1	LCK3_LEUMA	P21142 leucophaea

## ALIGNMENTS

```

RESULT 1
ACT7_SOYBN
ID ACT7_SOYBN STANDARD; PRT; 13 AA.
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ACTIN 7 (FRAGMENT).
GN SACT.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_Taxid=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. WAYNE;
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBICITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -1- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOSOLIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -1- SUBCELLULAR LOCATION: CYTOSOL.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X17120; CAA34980.1; -.
CC PIR: S15755; S15755.
CC InterPro: IPR000279; -.
CC PROSITE: PS00406; ACTINS_1; PARTIAL.
CC PROSITE: PS00432; ACTINS_2; PARTIAL.
CC PROSITE: PS01132; ACTINS_ACT_LIKE; PARTIAL.
CC Structural protein; Multigene family.
CC NON TER 13
CC SEQUENCE 13 AA: 1420 MW: 88EF3C36D4FD05A CRC64;

```

Query Match 18.2%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1; le+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 DIOP 11  
 |||  
 Db 6 DIOP 9

# RESULT 2

ACT6\_SOYBN STANDARD: PRT: 17 AA.  
 ID ACT6\_SOYBN  
 AC P15986;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ACTIN 6 (FRAGMENT).  
 GN SAG6.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1;  
 OC Fabales; Fabaceae; Papilionoideae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV\_MAYNE;  
 RX MEDLINE=9134640; PubMed=2102831;  
 RA Pearson L., Meagher R.B.;  
 RT "Diverse soybean actin transcripts contain a large intron in the 5'  
 RT untranslated leader: structural similarity to vertebrate muscle actin  
 RT genes";  
 RL Plant Mol. Biol. 14:513-526(1990).  
 CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
 CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBICUOUSLY EXPRESSED  
 CC IN ALL EUKARYOTIC CELLS.  
 CC -1- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN  
 CC IMPORTANT ROLE IN CYTOSOLIC STREAMING; CELL SHAPE DETERMINATION,  
 CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.  
 CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC  
 DR EMBL: X17119; CA34979.1; -;  
 DR PIR: S15754; S15754.  
 DR InterPro: IPR000279; -;  
 DR PROSITE: PS00406; ACTINS.1; PARTIAL.  
 DR PROSITE: PS00432; ACTINS.2; PARTIAL.  
 DR PROSITE: PS01132; ACTINS\_ACT\_LIKE; PARTIAL.  
 KW Structural protein; Multigene family.  
 FT NON\_TER 17  
 FT SEQUENCE 17 AA; 1749 MW; 38f4970d4bfff3c3 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 DIOP 11  
 |||  
 Db 6 DIOP 9

# RESULT 3

LOK1\_LOCM1 STANDARD: PRT: 6 AA.  
 ID LOK1\_LOCM1  
 AC P41491;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE LOCUSPAKININ I.  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera.  
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=9262851; PubMed=1585017;  
 RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,  
 RA de Loof A.;  
 RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,  
 RT isolation, primary structure and synthesis.";  
 RL Regul. Pept. 37:49-57(1992).  
 CC -1- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION  
 CC OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN  
 CC TUBULES.  
 DR PIR: A61068; A61068.  
 DR Neuropetide; Amidation.  
 KW MOD\_RES 6  
 FT SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 SSW 17  
 |||  
 Db 3 SSW 5

# RESULT 4

LANC\_CARUI STANDARD: PRT: 7 AA.  
 ID LANC\_CARUI  
 AC P36960;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE LANTIBIOTIC CARNOCIN U149 (FRAGMENT).  
 OS Carnobacterium sp. (strain U149).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;  
 OC Carnobacterium.  
 OX NCBI\_TaxID=35782;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92321768; PubMed=1622206;  
 RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
 RA Nes I.F.;  
 RT "Purification and characterization of a new bacteriocin isolated from  
 RT a Carnobacterium sp.";  
 RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
 CC -1- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).  
 CC ACTIVE ON GRAM-POSITIVE BACTERIA.  
 KW Antibiotic; Bacteriocin; Lantibiotic.  
 FT NON\_TER 7  
 FT SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 IOP 11  
 |||  
 Db 4 IOP 6

# RESULT 5

LCK2\_LEUMA STANDARD: PRT: 8 AA.  
 ID LCK2\_LEUMA  
 AC P21141;

DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 01-MAY-1991 (Rel. 18, Last annotation update)  
DE LEUCOKININ II (L-II).  
OS Leucophaea maderae (Madelira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
OC Blaberoidea; Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE AND SYNTHESIS.  
RC TISSUE-Head;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure and synthesis of two neuropeptides  
RT from Leucophaea maderae: members of a new family of  
RT Cephalomyotopsins.";  
RL Comp. Biochem. Physiol. 84C:205-211(1986).  
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.  
KM Neuropeptide; Amidation.  
FT MOD\_RES 8  
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match 13.6%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 SSW 17  
|||  
DB 5 SSW 7

RESULT 6  
LCK5\_LEUMA STANDARD; PRT; 8 AA.  
ID LCK5\_LEUMA  
AC P19987;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE LEUCOKININ V (L-V).  
OS Leucophaea maderae (Madelira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
OC Blaberoidea; Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE.  
RC TISSUE-Head;  
RX MEDLINE=87052651; PubMed=2877794;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
RT myotropic peptides of Leucophaea maderae.";  
RL Comp. Biochem. Physiol. 88C:27-30(1987).  
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.  
RC TISSUE-Head;  
PTR; JS0315; JS0315.  
KM Neuropeptide; Amidation.  
FT MOD\_RES 8  
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 SSW 17  
|||  
DB 5 SSW 7

RESULT 7  
LCK6\_LEUMA STANDARD; PRT; 8 AA.  
ID LCK6\_LEUMA  
AC P19988;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE LEUCOKININ VI (L-VI).  
OS Leucophaea maderae (Madelira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
OC Blaberoidea; Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE.  
RC TISSUE-Head;  
RX MEDLINE=87052651; PubMed=2877794;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
RT myotropic peptides of Leucophaea maderae.";  
RL Comp. Biochem. Physiol. 88C:27-30(1987).  
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND  
CC HELIOTHIS ZEA ADIOTROPIC HORMONE.  
DR PTR; JS0316; JS0316.  
KM Neuropeptide; Amidation.  
FT MOD\_RES 1  
FT MOD\_RES 8  
SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 QSS 16  
|||  
DB 1 QSS 3

RESULT 8  
LCK7\_LEUMA STANDARD; PRT; 8 AA.  
ID LCK7\_LEUMA  
AC P19987;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE LEUCOKININ VII (L-VII).  
OS Leucophaea maderae (Madelira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
OC Blaberoidea; Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE.  
RC TISSUE-Head;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure and synthesis of leucokinin VII and  
RT VIII: the final members of this new family of cephalomyotopic  
RT peptides isolated from head extracts of Leucophaea maderae.";  
RL Comp. Biochem. Physiol. 88C:31-34(1987).  
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.  
DR PTR; JS0317; JS0317.  
KM Neuropeptide; Amidation.  
FT MOD\_RES 8  
SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9C8676A CRC64;

Query Match 13.6%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 SSW 17  
|||

Db 5 SSW 7

## RESULT 9

OXYT\_BUFR

ID OXYT\_BUFR

AC P42995;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE SERITOCIN

OS Bufo regularis (African toad).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Bufonidae;

OC Bufo.

NCBI\_TaxID=8390;

RN [1]

RP SEQUENCE.

RC TISSUE=Plutitary neurointermediate lobe;

RX MEDLINE=96059313; PubMed=7591488;

RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;

RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),"

RL identified in a dryness-resistant African toad, Bufo regularis.";

CC Int. J. Pept. Protein Res. 45:482-487(1995).

CC -1- FUNCTION: DEVOID OF OXYTOCIN ACTIVITY.

CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR InterPro: IPR000981; "

DR Pfam: PF00220; hormone4; 1.

DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; FALSE\_NEG.

KW Hormone: Amidation.

FT DISULFID 1 6

FT MOD\_RES 9 9

SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match 13.6%; Score 3; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 IQS 15  
|||

Db 3 IQS 5

## RESULT 10

ULAH\_HUMAN

ID ULAH\_HUMAN

AC P31934;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE UNKNOWN PROTEIN FROM 2D-PAGE OF LIVER TISSUE (SPOT 94) (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=94147969; PubMed=8313870;

RA Hughes G.J., Fruiter S., Paquet N., Pasquali C., Sanchez J.-C.,

RT "Human liver protein map: update 1993."

RL Electrophoresis 14:1216-1222(1993).

CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC SWISS-2DPAGE: P31934; HUMAN.

FT NON\_TER 1 1

FT VARIANT 3 3

SQ SEQUENCE 10 AA; 1048 MW; 641D0DDAA723276B CRC64;

FT NON\_TER 9 9 /FTID=VAR\_000001.

FT SEQUENCE 9 AA; 990 MW; F10C7B172AB6DDCA CRC64;

SO SEQUENCE 9 AA; 990 MW; F10C7B172AB6DDCA CRC64;

Query Match 13.6%; Score 3; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AOD 8  
|||

Db 3 AOD 5

RESULT 11

PNEU\_HUMAN

ID PNEU\_HUMAN

AC P22103;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 01-AUG-1991 (Rel. 19, Last annotation update)

DE PNEUMADIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RC TISSUE=Lung;

RX MEDLINE=91110910; PubMed=2274681;

RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;

RT "Pneumadin: a new lung peptide which triggers antidiuresis.";

RL Regul. Pept. 30:77-87(1990).

CC -1- FUNCTION: ANTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.

DR PIR, B33143; B33143.

KW Amidation.

FT MOD\_RES 10 10

SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 13.6%; Score 3; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PKL 20  
|||

Db 4 PKL 6

## RESULT 12

PNEU\_RAT

ID PNEU\_RAT

AC P21996;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 01-AUG-1991 (Rel. 19, Last annotation update)

DE PNEUMADIN.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Rattus.

OC NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Lung;

RX MEDLINE=91110910; PubMed=2274681;

RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;

RT "Pneumadin: a new lung peptide which triggers antidiuresis.";

RL Regul. Pept. 30:77-87(1990).

CC -1- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.

DR PIR, A33143; A33143.

KW Amidation.

FT MOD\_RES 10 10

SQ SEQUENCE 10 AA; 1048 MW; 641D0DDAA723276B CRC64;



Query Match 13.6%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 Pkl 20  
 |||  
 Db 4 Pkl 6

RESULT 13  
 ID TM2A\_METMA STANDARD; PRT; 12 AA.  
 AC P80652;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE ALTERNATIVE TETRAHYDROMETHANOPTERIN S-METHYLTETRAHYDROMETHANOPTERIN  
 DE (EC 2.1.1.86) (N5-METHYLTETRAHYDROMETHANOPTERIN-COENZYME M  
 DE METHYLTETRAHYDROMETHANOPTERIN- (FRAGMENT).  
 OS Methanosarcina mazei.  
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;  
 OC Methanosarcina.  
 OX NCBI\_TaxID=2209;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=DSM 3647 / GOEL.  
 RA MEDLINE=96370840; PubMed=8774736;  
 RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;  
 RT "Sodium ion translocation by N5-methyltetrahydromethanopterin;  
 RT coenzyme M methyltransferase from Methanosarcina mazei Go1  
 RT reconstituted in ether lipid liposomes.";  
 RL Eur. J. Biochem. 239:857-864(1996).  
 CC -1- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN  
 CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND  
 CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-  
 CC TETRAHYDROMETHANOPTERIN.  
 CC -1- CATALYTIC ACTIVITY: 5-METHYL-5,6,7,8-TETRAHYDROMETHANOPTERIN +  
 CC 2-(METHYLTETRAHYDROMETHANOPTERIN) = 5,6,7,8-TETRAHYDROMETHANOPTERIN +  
 CC -1- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC Transferase; Methyltransferase; Transmembrane; Methanogenesis.  
 FT NON\_TER 12  
 FT SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 13.6%; Score 3; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 KLE 21  
 |||  
 Db 3 KLE 5

RESULT 14  
 ID CRTG\_BOVIN STANDARD; PRT; 13 AA.  
 AC P28489;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE CALRETIICULIN (CRP55) (CALREGULIN) (HACBP) (ERP60) (FRAGMENT).  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;

RX MEDLINE=91201375; PubMed=2016321;  
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,  
 RA Vance J.E., Opas M., Michalak M.;  
 RT "Calreticulin, and not calsequestrin, is the major calcium binding  
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 RT reticulum.";  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETIICULIN FAMILY.  
 DR PIR: A33208; A33208.  
 DR InterPro: IPR001580;  
 DR PROSITE: PS00803; CALRETIICULIN\_1; PARTIAL.  
 DR PROSITE: PS00804; CALRETIICULIN\_2; PARTIAL.  
 DR PROSITE: PS00805; CALRETIICULIN\_REPEAT; PARTIAL.  
 KW Endoplasmic reticulum; Calcium-binding.  
 FT NON\_TER 13  
 FT SEQUENCE 13 AA; 1557 MW; C85DDA6993CA1339 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 PAI 13  
 |||  
 Db 2 PAI 4

RESULT 15  
 ID HPAL\_RANES STANDARD; PRT; 13 AA.  
 AC P32415;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-OCT-1993 (Rel. 27, Last annotation update)  
 DE HEMOLYTIC PROTEIN A1 (FRAGMENT).  
 OS Rana esculenta (Edible frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 OX NCBI\_TaxID=8401;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90198965; PubMed=2317508;  
 RA Simmaco M., de Biase D., Severini C., Alta M., Ersamer G.F.,  
 RA Barra D., Bossa F.;  
 RT "Purification and characterization of bioactive peptides from skin  
 RT extracts of Rana esculenta.";  
 RL Biochim. Biophys. Acta 1033:318-323(1990).  
 CC -1- FUNCTION: SHOWS HEMOLYTIC ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: SECRETED.  
 CC -1- TISSUE SPECIFICITY: SKIN.  
 DR PIR: S09018; S09018.  
 KW Amphibian skin; Amidation; Hemolysis.  
 FT MOD\_RES 13  
 FT NON\_TER 13  
 FT SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 PAI 13  
 |||  
 Db 3 PAI 5

Job time: 511 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: July 23, 2001, 16:57:41 ; Search time 41.27 Seconds  
(Without alignments)  
40.607 Million cell updates/sec

Title: US-09-351-296-15

Perfect score: 22

Sequence: 1 QATROADIDQPAIQSSWPKLEQ 22

Scoring table: OLIGO

Searched: 219241 seqs, 76174552 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4035

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database:

PIR-68:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	18.2	13	2	actin 7 - soybean
2	4	18.2	14	2	T-cell receptor al
3	4	18.2	17	2	actin 6 - soybean
4	4	18.2	18	2	13K protein 5306 l
5	4	18.2	22	2	folate binding pro
6	4	18.2	22	2	folate binding pro
7	3	13.6	6	2	phosphoglycerate t
8	3	13.6	6	2	locustakinin - mig
9	3	13.6	7	2	peptidyl-di-peptida
10	3	13.6	7	2	carnocin u149 - Ca
11	3	13.6	8	2	leucokinin V - Mad
12	3	13.6	8	2	leucokinin VI - Ma
13	3	13.6	9	2	adipokinetic hormo
14	3	13.6	9	2	spectrin alpha cha
15	3	13.6	10	2	pneumadin - huma
16	3	13.6	10	2	pneumadin - rat
17	3	13.6	10	2	Ig heavy chain CRD
18	3	13.6	10	2	collagen alpha 1(V
19	3	13.6	10	2	unidentifiled 5.7/3
20	3	13.6	11	2	spermathesisin AON-3
21	3	13.6	11	2	foliistatin - bovi
22	3	13.6	12	2	T-cell receptor be
23	3	13.6	12	2	T-cell receptor be
24	3	13.6	12	2	hypothetical prote
25	3	13.6	12	2	Ig heavy chain CRD
26	3	13.6	12	2	Ig heavy chain DJ
27	3	13.6	12	2	T-cell receptor be
28	3	13.6	12	2	T-cell receptor de
29	3	13.6	12	2	

30	3	13.6	12	2	C20907	Ig kappa-1 chain J
31	3	13.6	12	2	F20907	Ig kappa-2 chain J
32	3	13.6	13	2	A33208	calreticulin, hepa
33	3	13.6	13	2	S09018	hemolytic protein
34	3	13.6	13	2	A57789	galbladder stone
35	3	13.6	13	2	B61458	Ig kappa chain V-I
36	3	13.6	13	2	S10562	Ig kappa chain V-I
37	3	13.6	13	2	C53275	zona pellucida-bin
38	3	13.6	13	2	E53275	Ig kappa-1 chain J
39	3	13.6	13	2	H33952	Ig kappa-1 chain J
40	3	13.6	13	2	A33933	Ig kappa chain J r
41	3	13.6	13	2	B26406	Ig kappa chain J r
42	3	13.6	13	2	A47630	Ig kappa chain J r
43	3	13.6	13	2	C47630	Ig kappa chain J r
44	3	13.6	13	2	B47630	Ig kappa chain J r
45	3	13.6	13	2		

## ALIGNMENTS

RESULT 1  
S15755  
actin 7 - soybean (fragment)  
C:Species: Glycine max (soybean)  
C>Date: 20-Feb-1995 #sequence\_revision 29-May-1998 #text\_change 13-Aug-1999  
C:Accession: S15755  
R:Pearson, L.; Meagher, R.B.  
Plant Mol. Biol. 14, 513-526, 1990  
A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated  
A:Reference number: S15754; MUID:91346640  
A:Accession: S15755  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-13 <PEAK>  
A:Cross-references: EMBL:X17120; NID:g18527; PIDN:CAA34980.1; PID:g18528  
A:Superfamily: actin  
C:Keywords: cytoskeleton; structural protein

Query Match 18.2%; Score 4; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 8 DIOP 11  
Db 6 DIOP 9

RESULT 2  
PT0210  
T-cell receptor alpha chain V-J region (4-1-K.1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997  
C:Accession: PT0210  
R:Nakano, N.; Kikuchi, H.; Nishimoto, H.; Kishimoto, T.  
J. Exp. Med. 173, 1091-1097, 1991  
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not rest  
A:Reference number: PT0209; MUID:91217621  
A:Accession: PT0210  
A:Molecule type: mRNA  
A:Residues: 1-14 <NAK>  
C:Keywords: T-cell receptor

Query Match 18.2%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 2 ATRO 5  
Db 6 ATRO 9

RESULT 3  
S15754  
actin 6 - soybean (fragment)  
C:Species: Glycine max (soybean)  
C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: S15754; S08049  
R:Pearson, L.; Meagher, R.B.  
Plant Mol. Biol. 14, 513-526, 1990  
A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated  
A:Reference number: S15754; MUID:91346640  
A:Accession: S15754  
A:Molecule type: DNA  
A:Residues: 1-17 <PEA>  
A:Cross-references: EMBL:X17119; NID:g18525; PIDN:CMA34979.1; PID:g18526  
C:Superfamily: actin  
C:Keywords: cytoskeleton

Query Match 18.2%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 DIOP 11  
Db 6 DIOP 9

RESULT 4  
A38890  
13K protein 5306 [imported] - rice (strain Nihonbare) (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 20-Apr-2000  
C:Accession: A38890; PS0206  
R:Tsugita, A.; Kamo, M.  
Submitted to JIPID, April 1993  
A:Reference number: PS0209  
A:Accession: A38890  
A:Molecule type: protein  
A:Residues: 1-18 <TSU>  
A:Experimental source: leaf, chloroplast, strain Nihonbare  
A:Note: molecular weight 13k, pI 5.1

Query Match 18.2%; Score 4; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PAIQ 14  
Db 4 PAIQ 7

RESULT 5  
S62669  
folate binding protein I - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S62669  
R:da Costa, M.; Rothenberg, S.P.  
Biochim. Biophys. Acta 1292, 23-30, 1996  
A:Title: Purification and characterization of folate binding proteins from rat placenta.  
A:Reference number: S62669; MUID:96139323  
A:Accession: S62669  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-22 <DAC>

Query Match 18.2%; Score 4; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QATR 4  
Db 1 QATR 4

RESULT 6  
S62670  
folate binding protein II - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S62670  
R:da Costa, M.; Rothenberg, S.P.  
Biochim. Biophys. Acta 1292, 23-30, 1996  
A:Title: Purification and characterization of folate binding proteins from rat placenta  
A:Reference number: S62669; MUID:96139323  
A:Accession: S62670  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-22 <DAC>

Query Match 18.2%; Score 4; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QATR 4  
Db 1 QATR 4

RESULT 7  
T11779  
phosphoglycerate transport regulatory protein pgfA - Salmonella typhimurium (fragment)  
C:Species: Salmonella typhimurium  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: T11779  
R:Yang, Y.L.; Goldrick, D.; Hong, J.S.  
J. Bacteriol. 170, 4299-4303, 1988  
A:Title: Identification of the products and nucleotide sequences of two regulatory genes  
A:Reference number: Z17339; MUID:88314933  
A:Accession: T11779  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <YAN>  
A:Cross-references: EMBL:M21279; NID:g858752; PID:g154260  
A:Experimental source: strain LT2

Query Match 13.6%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LEQ 22  
Db 2 LEQ 4

RESULT 8  
A61068  
locustakinin - migratory locust  
C:Species: Locusta migratoria (migratory locust)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 08-Dec-1995  
C:Accession: A61068  
R:Schroofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.  
Regul. Pept. 37, 49-57, 1992  
A:Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation,  
A:Reference number: A61068; MUID:92262851  
A:Accession: A61068  
A:Molecule type: protein  
A:Residues: 1-6 <SCH>  
C:Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide  
F:6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 SSW 17  
|||  
Db 3 SSW 5

RESULT 9  
JN0859  
peptidyl-diesterase A inhibitory peptide C105 - striped bonito

C:Species: Sarda orientalis (striped bonito)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999

C:Accession: JN0859  
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.

Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993

A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe

A:Reference number: JN0859; MUID:94080036

A:Accession: JN0859

A:Molecule type: protein

A:Residues: 1-7 <MAT>

A:Experimental source: intestine  
A:Comment: The carboxyl-terminus is essential for the protease's expression of angiotensin

C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 13.6%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 KLE 21  
|||  
Db 4 KLE 6

RESULT 10

A58718  
carnocin U149 - Carnobacterium sp. (fragment)

C:Species: Carnobacterium sp.

C:Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998

C:Accession: A58718

R:Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.

Appl. Environ. Microbiol. 58, 1417-1422, 1992

A:Title: Purification and characterization of a new bacteriocin isolated from a Carnobac

A:Reference number: A58718; MUID:92321768

A:Accession: A58718

A:Molecule type: protein

A:Status: preliminary

A:Residues: 1-7 <STO>  
C:Keywords: antibiotic; lanthionine

Query Match 13.6%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 IOP 11  
|||  
Db 4 IOP 6

RESULT 11

JS0315  
leucokinin V - Madeira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000

C:Accession: JS0315

R:Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 27-30, 1987

A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic

A:Reference number: JS0315  
A:Accession: JS0315

A:Molecule type: Protein

A:Residues: 1-8 <HOL>

C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile

C:Keywords: amidated carboxyl end; cephalomyotropic peptide

F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 SSW 17  
|||  
Db 5 SSW 7

RESULT 12  
JS0316

leucokinin VI - Madeira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000

C:Accession: JS0316

R:Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 27-30, 1987

A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotrop

A:Reference number: JS0315

A:Accession: JS0316

A:Molecule type: Protein

A:Residues: 1-8 <HOL>

C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile

C:Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 QSS 16  
|||  
Db 1 QSS 3

RESULT 13  
JS0317

leucokinin VII - Madeira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000

C:Accession: JS0317

R:Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 31-34, 1987

A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII: the

A:Reference number: JS0317

A:Accession: JS0317

A:Molecule type: protein

A:Residues: 1-8 <HOL>  
C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile

C:Keywords: amidated carboxyl end; cephalomyotropic peptide

F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 SSW 17  
|||  
Db 5 SSW 7

## RESULT 14

A24244

adipokinetin hormone - bollworm

N:Alternate names: Hez-AKH

C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)

C:Date: 31-Mar-1988 #sequence\_revision 23-Mar-1995 #text\_change 31-Oct-1997

C:Accession: A24244

R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway

Biochem. Biophys. Res. Commun. 135, 622-628, 1986

A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio-

A:Reference number: A24244; MUID:86186794

A:Accession: A24244

A:Molecule type: protein

A:Residues: 1-9 &lt;JAF&gt;

C:Superfamily: adipokinetin hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:9/Modified site: amidated carboxyl end (Gly) #status experimental

## Query Match

13.6%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 SSW 17

|||

Db 6 SSW 8

## RESULT 15

PC7076

spectrin alpha chain, non-erythroid - mouse (fragment)

N:Alternate names: fodrin alpha chain

C:Species: Mus musculus (house mouse)

C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000

C:Accession: PC7076

R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;

Electrophoresis 21, 1853-1871, 2000

A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t

A:Reference number: PC7072

A:Accession: PC7076

A:Molecule type: protein

A:Residues: 1-9 &lt;TSU&gt;

A:Experimental source: strain C57BL/6Cr SLC, male; brain, striatum

C:Keywords: brain

## Query Match

13.6%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATR 4

|||

Db 3 ATR 5

Search completed: July 23, 2001, 16:57:41  
Job time: 283 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: July 23, 2001, 16:56:53 ; Search time 34.6 Seconds  
(without alignments)  
12.809 Million cell updates/sec

Title: US-09-351-296-15

Perfect score: 22

Sequence: 1 QATRQAQDIQPAIQSSWPKLEQ 22

Scoring table: OLIGO

Searched: 193259 seqs, 20144635 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93443

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2.6/prodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2.6/prodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2.6/prodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2.6/prodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2.6/prodata/2/1aa/PCTUS.COMB.pep.\*  
6: /cgn2.6/prodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	2	US-08-845-926-15
2	8	36.4	22	2	US-08-146-028-98
3	8	36.4	22	2	US-08-845-926-14
4	8	36.4	22	4	US-08-723-425A-98
5	6	36.4	22	4	US-09-112-206-98
6	5	22.7	21	1	US-08-071-811A-7
7	5	22.7	21	2	US-08-442-461D-26
8	4	18.2	6	2	US-08-893-853-7
9	4	18.2	7	3	US-08-863-118-14
10	4	18.2	7	4	US-09-113-921-7
11	4	18.2	8	2	US-08-616-669A-20
12	4	18.2	8	3	US-08-335-733D-70
13	4	18.2	8	3	US-08-335-733D-71
14	4	18.2	8	3	US-08-335-733D-72
15	4	18.2	8	3	US-08-335-733D-73
16	4	18.2	8	3	US-08-335-733D-74
17	4	18.2	8	4	US-09-326-440-20
18	4	18.2	9	2	US-08-232-081B-6
19	4	18.2	9	3	US-08-159-339A-389
20	4	18.2	9	3	US-08-335-733D-6
21	4	18.2	9	4	US-09-113-921-56
22	4	18.2	9	4	US-09-113-921-118
23	4	18.2	10	1	US-08-306-116A-38
24	4	18.2	10	2	US-08-637-759B-271
25	4	18.2	10	3	US-08-871-355A-271
26	4	18.2	11	3	US-08-105-904B-13
27	4	18.2	12	1	US-08-376-362A-19

28	4	18.2	13	2	US-08-893-853-45	Sequence 45, App1
29	4	18.2	13	4	US-09-113-921-45	Sequence 45, App1
30	4	18.2	14	2	US-08-442-461D-1	Sequence 1, App1
31	4	18.2	14	2	US-08-765-783A-93	Sequence 93, App1
32	4	18.2	14	2	US-08-765-783A-96	Sequence 96, App1
33	4	18.2	14	2	US-08-765-783A-103	Sequence 103, App1
34	4	18.2	15	3	US-09-141-882A-6	Sequence 6, App1
35	4	18.2	15	1	US-08-156-552A-22	Sequence 22, App1
36	4	18.2	15	4	US-09-035-249A-22	Sequence 22, App1
37	4	18.2	16	1	US-08-164-618-18	Sequence 18, App1
38	4	18.2	16	1	US-08-133-011-143	Sequence 143, App1
39	4	18.2	16	1	US-08-326-117B-20	Sequence 20, App1
40	4	18.2	16	2	US-08-902-623-6	Sequence 6, App1
41	4	18.2	16	3	US-08-982-129-20	Sequence 20, App1
42	4	18.2	16	3	US-08-806-597A-12	Sequence 12, App1
43	4	18.2	16	3	US-08-970-428A-12	Sequence 12, App1
44	4	18.2	16	4	US-08-907-739-143	Sequence 143, App1
45	4	18.2	17	1	US-08-071-811A-1	Sequence 1, App1

## ALIGNMENTS

RESULT 1  
US-08-845-926-15  
Sequence 15, Application US/08845926  
Patent No. 5935778  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike  
APPLICANT: SCHMITT, Urban  
APPLICANT: JUNG, G. nher-Gerhard  
APPLICANT: IHLENFELDT, HANS-Georg  
TITLE OF INVENTION: Method for serological typing using  
TITLE OF INVENTION: type-specific antigens  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845,926  
FILING DATE: 04-28-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/598,993  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 04 302.2  
FILING DATE: 09-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:

ORGANISM: Hepatitis C Virus  
US-08-845-926-15

Query Match 100.0%; Score 22; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 7.3e-18;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QATROADIODIOPAIOSMPKLEO 22  
Db 1 QATROADIODIOPAIOSMPKLEO 22

RESULT 2  
US-08-146-028-98  
Sequence 98, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,028  
INFORMATION FOR SEQ ID NO: 98:

SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1

FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 22  
US-08-146-028-98

Query Match 36.4%; Score 8; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 QAODIOPA 12  
Db 14 QAODIOPA 21

RESULT 3  
US-08-845-926-14  
Sequence 14, Application US/0845926  
Patent No. 5935778  
GENERAL INFORMATION:

APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike  
APPLICANT: SCHMITT, Urban  
APPLICANT: JUNG, G ather-Gerhard  
APPLICANT: IHLENFELDT, HANS-Georg  
APPLICANT: KRAAS, Wolfgang  
TITLE OF INVENTION: Method for serological typing using  
TITLE OF INVENTION: type-specific antigens  
NUMBER OF SEQUENCES: 46

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.  
ZIP: 20005-5701

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/845,926  
FILING DATE: 04-28-1997  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/598,993  
FILING DATE: 09-FEB-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 04 302.2  
FILING DATE: 09-FEB-1995  
ATTORNEY/AGENT INFORMATION:

NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS:

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:

ORGANISM: Hepatitis C Virus  
US-08-845-926-14

Query Match 36.4%; Score 8; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 QAODIOPA 12  
Db 5 QAODIOPA 12

RESULT 4  
US-08-723-425A-98  
Sequence 98, Application US/08723425A  
Patent No. 6165730  
GENERAL INFORMATION:

APPLICANT: DELEYS, ROBERT  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
NUMBER OF SEQUENCES: 453  
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/723,425A  
FILING DATE: 435  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B. J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
NAME/KEY: Modified-site  
LOCATION: 22  
US-08-723-425A-98

Query Match 36.4%; Score 8; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QAQDIQPA 12  
|||||||  
Db 14 QAQDIQPA 21

RESULT 5  
US-09-112-206-98  
Sequence 98, Application US/09112206  
Patent No. 6210903  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINILATED  
PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/112,206  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/146,028  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
FEATURE:

NAME/KEY: Modified-site  
LOCATION: 22  
US-09-112-206-98

Query Match 36.4%; Score 8; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QAQDIQPA 12  
|||||||  
Db 14 QAQDIQPA 21

RESULT 6  
US-08-071-811A-7  
Sequence 7, Application US/08071811A  
Patent No. 5654398  
GENERAL INFORMATION:  
APPLICANT: Frankel, Alan  
APPLICANT: Tan, Ruoying  
TITLE OF INVENTION: Compositions and Methods for Inhibiting  
TITLE OF INVENTION: Replication of Human Immunodeficiency Virus-1  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/071,811A  
FILING DATE: 03-JUN-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Heslin, James M.  
REGISTRATION NUMBER: 29,541  
REFERENCE/DOCKET NUMBER: 2307U-044200  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-071-811A-7

Query Match 22.7%; Score 5; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATROA 6  
|||||  
Db 4 ATROA 8

RESULT 7  
US-08-442-461D-26  
Sequence 26, Application US/08442461D  
Patent No. 5834184  
GENERAL INFORMATION:  
APPLICANT: Harada, Kazuo

APPLICANT: Martin, Shelley S.  
APPLICANT: Frankel, Alan  
TITLE OF INVENTION: In Vivo Selection of RNA-Binding  
Peptides  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,461D  
FILING DATE: 17-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschuetz, Joe  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 02307U-060500US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-442-461D-26

Query Match 22.7%; Score 5; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATROA 6  
|||||  
Db 2 ATROA 6

RESULT 8  
US-08-893-853-7  
Sequence 7, Application US/08893853  
Patent No. 5891994  
GENERAL INFORMATION:  
APPLICANT: Goldstein, Gideon  
TITLE OF INVENTION: Methods and Compositions for Impairing  
TITLE OF INVENTION: Multiplication of HIV-1  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr., P.O. Box 457  
CITY: Spring House  
STATE: PA  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,853  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GGP2USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-893-853-7

Query Match 18.2%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1,4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PKLE 21  
|||||  
Db 2 PKLE 5

RESULT 9  
US-08-863-118-14  
Sequence 14, Application US/08863118A  
Patent No. 6015893  
GENERAL INFORMATION:  
APPLICANT: CANCE, William G.  
APPLICANT: LIU, Edison T.  
TITLE OF INVENTION: Oligonucleoside Compounds and Methods for Inhibiting  
TITLE OF INVENTION: Tumor Growth, Invasion and Metastasis  
FILE REFERENCE: 3470-90  
CURRENT APPLICATION NUMBER: US/08/863,118A  
CURRENT FILING DATE: 1997-05-27  
EARLIER APPLICATION NUMBER: 08/276,843  
EARLIER FILING DATE: 1994-07-18  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 14  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: portion of  
OTHER INFORMATION: focal adhesion kinase protein  
US-08-863-118-14

Query Match 18.2%; Score 4; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1,4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 QSSW 17  
|||||  
Db 2 QSSW 5

RESULT 10  
US-09-113-921-7  
Sequence 7, Application US/09113921  
Patent No. 6193981  
GENERAL INFORMATION:  
APPLICANT: Goldstein, Gideon  
TITLE OF INVENTION: Methods and Compositions for Impairing  
TITLE OF INVENTION: Multiplication of HIV-1  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr., P.O. Box 457

CITY: Spring House  
STATE: PA  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/113,921  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/893,853  
FILING DATE: 11-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GSP2AUSA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-113-921-7

Query Match 18.2%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PKLE 21  
||||  
Db 3 PKLE 6

RESULT 11  
US-08-616-669A-20  
Sequence 20 Application US/08616669A  
Patent No. 5948765  
GENERAL INFORMATION:  
APPLICANT: Muslim, Anthony J.  
TITLE OF INVENTION: Inhibition of Intracellular Signal  
TRANSDUCTION BY 14-3-3-BINDING PEPTIDES  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howell & Haferkamp, L.C.  
STREET: 7733 Forsyth Boulevard, Suite 1400  
CITY: St. Louis  
STATE: MO  
COUNTRY: US  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/616,669A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Holland, Donald R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 964064  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note= "A phosphorylated tyrosine"  
US-08-616-669A-20

Query Match 18.2%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 IQPA 12  
||||  
Db 4 IQPA 7

RESULT 12  
US-08-335-733D-70  
Sequence 70 Application US/08335733D  
Patent No. 6042831  
GENERAL INFORMATION:  
APPLICANT: Beretta, Alberto  
TITLE OF INVENTION: HIV PROTEIN EPITOPES  
NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Baker & Botts, L.L.P.  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,733D  
FILING DATE: 10-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Macleod, Janet M.  
REGISTRATION NUMBER: 35,263  
REFERENCE/DOCKET NUMBER: A29928-PCT-USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2500  
TELEFAX: 212-765-2519  
TELEX:  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-335-733D-70

Query Match 18.2%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 R0AQ 7  
1111  
Db 5 R0AQ 8

RESULT 13  
US-08-335-733D-71  
; Sequence 71, Application US/08335733D  
; Patent No. 6042831  
; GENERAL INFORMATION:  
; APPLICANT: Beretta, Alberto  
; TITLE OF INVENTION: HIV PROTEIN EPITOPES  
; TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Baker & Botts, L.L.P.  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10112-0228  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,733D  
; FILING DATE: 10-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacLeod, Janet M  
; REGISTRATION NUMBER: 35,263  
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-408-2500  
; TELEFAX: 212-765-2519  
; TELEX:  
; INFORMATION FOR SRO ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: Internal  
; ORIGINAL SOURCE:  
US-08-335-733D-71

Query Match 18.2%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 R0AQ 7  
1111  
Db 4 R0AQ 7

RESULT 14  
US-08-335-733D-72  
; Sequence 72, Application US/08335733D

; Patent No. 6042831  
; GENERAL INFORMATION:  
; APPLICANT: Beretta, Alberto  
; TITLE OF INVENTION: HIV PROTEIN EPITOPES  
; TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Baker & Botts, L.L.P.  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10112-0228  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,733D  
; FILING DATE: 10-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacLeod, Janet M  
; REGISTRATION NUMBER: 35,263  
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-408-2500  
; TELEFAX: 212-765-2519  
; TELEX:  
; INFORMATION FOR SRO ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: Internal  
; ORIGINAL SOURCE:  
US-08-335-733D-72

Query Match 18.2%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 R0AQ 7  
1111  
Db 3 R0AQ 6

RESULT 15  
US-08-335-733D-73  
; Sequence 73, Application US/08335733D  
; Patent No. 6042831  
; GENERAL INFORMATION:  
; APPLICANT: Beretta, Alberto  
; TITLE OF INVENTION: HIV PROTEIN EPITOPES  
; TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Baker & Botts, L.L.P.  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10112-0228  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,733D  
FILING DATE: 10-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacLeod, Janet M  
REGISTRATION NUMBER: 35,263  
REFERENCE/DOCKET NUMBER: A29928-PCT-USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2500  
TELEFAX: 212-765-2519  
TELEX:  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
US-08-335-733D-73

Query Match 18.28; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ROAQ 7  
Db 2 ROAQ 5

Search completed: July 23, 2001, 16:56:53  
Job time: 270 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: July 23, 2001, 16:56:12 ; Search time 65.41 Seconds  
(without alignments)  
20.390 Million cell updates/sec

Title: US-09-351-296-15

Perfect score: 22  
Sequence: 1 QATRQMDIQPAIQSSWPKLEQ 22

## Scoring table:

OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 148088

Minimum DB seq length: 6  
Maximum DB seq length: 22

## Post-processing: Listing first 45 summaries

## Database :

A\_Geneseq\_0601:\*

1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:\*

2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:\*

3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:\*

4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:\*

5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:\*

6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:\*

7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT:\*

8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT:\*

9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT:\*

10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:\*

11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:\*

12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:\*

13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:\*

14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:\*

15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:\*

16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:\*

17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:\*

18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:\*

19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:\*

20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:\*

21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:\*

22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	100.0	22	17	AA999905	Hepatitis C Virus
2	8	36.4	22	14	AA941155	HCV (type 2) pepti
3	8	36.4	22	17	AA999904	Hepatitis C Virus
4	5	22.7	10	18	AA915796	Adherence factor p
5	5	22.7	12	13	AA925629	Ras 126-137 -contr
6	5	22.7	22	17	AA995551	Hepatitis C Virus
7	4	18.2	6	19	AA956941	Enzyme inhibitor p
8	4	18.2	6	19	AA956958	Enzyme inhibitor p
9	4	18.2	7	20	AA905076	HIV Tat protein ep
10	4	18.2	7	22	AA987883	Epitope I peptide
11	4	18.2	8	16	AA973549	Human TSH receptor

12	4	18.2	8	16	AA973551	Human TSH receptor
13	4	18.2	8	19	AA959591	Epitope of the Hep
14	4	18.2	9	14	AA937604	hIL2R Ab L chain V
15	4	18.2	9	14	AA942576	HLA epitope. Homo
16	4	18.2	9	15	AA938090	Hepatitis B virus-
17	4	18.2	9	17	AA949589	Human leucocyte an
18	4	18.2	9	18	AA945662	HBV pol 398 peptid
19	4	18.2	9	20	AA945658	Immunogenic peptid
20	4	18.2	9	20	AA946619	Immunogenic peptid
21	4	18.2	9	20	AA946696	Immunogenic peptid
22	4	18.2	9	20	AA950184	HIV Tat protein ep
23	4	18.2	9	20	AA950100	HIV Tat protein ep
24	4	18.2	9	21	AA998532	WT1 derived immuno
25	4	18.2	9	21	AA998557	WT1 derived immuno
26	4	18.2	9	21	AA998617	WT1 derived immuno
27	4	18.2	9	21	AA998655	WT1 derived immuno
28	4	18.2	9	21	AA998683	WT1 derived immuno
29	4	18.2	9	22	AA987932	Immunogen #1. Unl
30	4	18.2	9	22	AA987994	Epitope peptide #1
31	4	18.2	10	19	AA923886	HIV-1 peptide 1987
32	4	18.2	10	20	AA946822	Immunogenic peptid
33	4	18.2	10	21	AA973069	Hepatitis B virus
34	4	18.2	11	15	AA960845	COSM precursor pol
35	4	18.2	11	19	AA962143	Haemophilus influe
36	4	18.2	11	21	AA959623	Human collagen 18
37	4	18.2	12	19	AA934530	Alpha epithelial s
38	4	18.2	13	19	AA938444	Neuropeptide y rec
39	4	18.2	13	19	AA938445	Neuropeptide y rec
40	4	18.2	13	19	AA938446	Neuropeptide y rec
41	4	18.2	13	19	AA938450	Neuropeptide y rec
42	4	18.2	13	19	AA938433	Neuropeptide y rec
43	4	18.2	13	19	AA938441	Neuropeptide y rec
44	4	18.2	13	20	AA950209	Neutrophil activat
45	4	18.2	13	20	AA950134	HIV Tat protein ep

## ALIGNMENTS

RESULT 1

AA999905

ID AAR99905 standard; peptide: 22 AA.

XX

AC AAR99905;

XX

DT 23-APR-1997 (first entry)

XX

DE Hepatitis C Virus antigen peptide 15.

XX

KW HCV; immunologically reactive; antigen; epitope; screen; typing;

KW antibody; Immobilised.

XX

OS Hepatitis C Virus.

XX

PN EP726463-A2.

XX

PD 14-AUG-1996.

XX

PF 09-FEB-1996; 96EP-0101925.

XX

PR 09-FEB-1995; 95DE-4004302.

XX

PA (BOEF ) BOEHRINGER MANNHEIM GMBH.

XX

PI Schmitt U, Seidel C, Wienhues-Chelen U;

XX

DR WPI; 1996-364504/37.

XX

PT Antibody typing by sequential reaction with immobilised antigens -

PT esp. using new hepatitis C virus peptide(s) as antigens

XX

PS Claim 9; Page 15; 22pp; German.

XX





SQ Sequence 22 AA;

Query Match 36.4%; Score 8; DB 17; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.045;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 OAODIOPA 12  
 |||||  
 Db 5 qaqdtqpa 12

## RESULT 4

AAW15796  
 ID AAW15796 standard; Peptide: 10 AA.

AC AAW15796;

DT 19-JAN-1998 (first entry)

DE Adherence factor peptide.

KW Adherence factor; adhesin; class II solute transporter; mucosa;  
 GRAS; probiotic; screening; food additive.

OS Synthetic.

PN WO9714802-A1.

PD 24-APR-1997.

PF 21-OCT-1996; 96WO-NL00409.

PR 20-OCT-1995; 95WO-NL00367.

PA (NEDE ) NEDERLANDSE ORG TOEGEPAST.

PI Conway PL, Leer RJ, Pouwels PH;

DR WPI; 1997-245117/22.

PT Adherence factors of non-pathogenic microorganisms - useful for  
 screening for microorganisms and as food additives

PS Claim 6; Page 29; 49pp; English.

CC A novel claimed protein (A) from a non-pathogenic microorganism  
 CC has mucosa binding promoting (MBP) activity and is characterised  
 CC as including peptide motifs at least 80% similar, and preferably  
 CC more than 90% similar, to the peptide sequences I-V given in  
 CC AAW15794-98, especially to peptides II-V. (A) preferably also  
 CC includes a conserved consensus motif (see AAW26577) and one or both  
 CC of 2 claimed consensus sequences (see AAW15792 and AAW15793). Such  
 CC adherence factors, e.g. 104R adherence factor of *Lactobacillus*  
 CC fermentum (see AAW15799), can be used for prophylaxis and/or treatment  
 CC of disease or illness associated with a mucosa-colonising pathogens.  
 CC The part expressing MBP activity is useful as a targeting  
 CC component for an additional pharmaceutical component physically  
 CC linked to the targeting component. Compositions comprising the  
 CC adherence factors are useful for improving food products.  
 CC Detection of the genes or proteins is useful for screening for  
 CC non-pathogenic microorganisms.

SQ Sequence 10 AA;

Query Match 22.7%; Score 5; DB 18; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 33;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 AIGSS 16  
 |||||  
 Db 3 aigss 7

## RESULT 5

AAAR25629  
 ID AAR25629 standard; peptide: 12 AA.

AC AAR25629;

DT 20-JAN-1993 (first entry)

DE Ras 126-137 -control peptide showing no Ras inhibition.

KW GRPase; activating protein; GAP; oncogenesis; cancer; truncated;  
 colorectal; exocrine pancreatic; myeloid leukaemia; adenyl acylase.

OS Synthetic.

PN EP496162-A.

PD 29-JUL-1992.

PF 16-DEC-1991; 91EP-0311658.

PR 24-DEC-1990; 90US-0632891.

PA (MERI ) MERCK &amp; CO INC.

PI Freidinger RM, Garsky VM, Gibbs JB, Schaber MD, Sigal IS;

DR WPI; 1992-251427/31.

PT Synthetic peptide inhibitors of Ras-GAP interaction - as  
 PT antitumour agents against e.g. colorectal carcinoma, exocrine  
 PT pancreatic carcinoma and myeloid leukaemia

PS Disclosure; Page 11; 31pp; English.

CC The peptide corresponds to the prod. of the Harvey ras oncogene  
 CC from residues 126-137. The peptide is used as a negative control in  
 CC the study of peptides which bind to GRPase activating protein (GAP)  
 CC thus inhibiting Ras activation by GAP and inhibiting Ras-dependent  
 CC cell transformation. Oncogenic forms of Ras occur in various human  
 CC cancers, e.g. colorectal carcinoma, exocrine pancreatic carcinoma  
 CC and myeloid leukaemias. Ras complexed with GTP can bind GAP and  
 CC this is thought to be the important step in the transformation  
 CC activity of Ras. See also AAR25602-28.

SQ Sequence 12 AA;

Query Match 22.7%; Score 5; DB 13; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ROAOD 8  
 |||||  
 Db 3 rqaqd 7

## RESULT 6

AAAR95551  
 ID AAR95551 standard; Peptide: 22 AA.

AC AAR95551;

DT 26-SEP-1996 (first entry)

DE Hepatitis C Virus II Non-structural protein 4 epitope.

KW HCV; hepatitis C virus; epitope; antigen; detection; chimera.

OS Hepatitis C virus.  
 XX

CC The present sequence represents an enzyme inhibitor peptide used in

CC The present sequence represents an enzyme inhibitor peptide used in

the method of the invention to distinguish between t-PA and u-PA. The

CC present invention describes a substrate subtraction library for the  
CC identification of peptide substrates selective between a first enzyme  
CC (E1) and a second enzyme (E2), comprising a collection of different  
CC peptides, substantially lacking peptides that are effective substrates  
CC for E1. Also described are: (1) a method (M1) for identifying peptide  
CC substrates selective between a first enzyme (E1) and a second enzyme  
CC (E2); (2) a compound comprising the amino acid sequence of a peptide  
CC identified by M1; (3) a polypeptide for use as an enzyme inhibitor  
CC comprising one of 237 amino acid sequences (see AAM56801 to AAM56947,  
CC and AAM5649 to AAM57038); (4) a recombinant DNA vector comprising DNA  
CC (1) encoding a protease inhibitor including the sequence identified by  
CC the M1; (5) a prokaryotic or eukaryotic cell containing the vector of  
CC (4); (6) an antibody (Ab) immunoreactive with at least one of the  
CC peptides identified by M1; and (7) a diagnostic assay for distinguishing  
CC between active and latent forms of protease inhibitors, that uses (Ab).  
CC The library and method are used for distinguishing between active and  
CC latent forms of enzyme inhibitors, e.g. proteases, kinases and  
CC phosphatases. (Ab) are used for affinity purification of recombinant  
CC peptides and in the identification of naturally occurring protease  
CC inhibitors. Enzyme-inhibiting peptides identified can be used to treat a  
CC serpin deficiency or a disorder of serine proteases.

SO Sequence 6 AA;

Query Match 18.2%; Score 4; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ROAQ 7  
|||  
Db 3 rgaq 6

RESULT 9

AAV05076  
ID AAV05076 standard; peptide: 7 AA.

AAV05076;

16-JUN-1999 (first entry)

HIV Tat protein epitope peptide SEQ ID NO 7.

HIV: Tat protein; epitope: human immunodeficiency virus; immune response;  
viral multiplication reduction; chronic viraemia.

Human immunodeficiency virus type 1.

Key 1 Location/Qualifiers

Modified-site 1 /note= "N-terminus can optionally be modified with  
hydrogen, a lower alkyl, a lower alkanoyl, or a  
sequence of 1 to 5 amino acids optionally  
substituted with a lower alkyl or lower alkanoyl"

Modified-site 7 /note= "C-terminus can optionally be modified with a free  
hydroxyl, an amide, or a sequence of up to 14  
amino acids optionally substituted with an amide"

WO9902185-A1.

21-JAN-1999.

10-JUL-1998; 98WO-US14332.

11-JUL-1997; 97US-0893853.

(THYM-) THYMON LLC.

Goldstein G;

WPI; 1999-120516/10.

XX Peptides containing epitopes of human immune deficiency virus Tat  
PT protein - used to induce antibodies reacting with HIV-1 Tat  
PT proteins, used to, e.g. reduce HIV-1 levels in both infected and  
PT uninfected patients

Claim 5; Page 119; 140pp; English.

XX This sequence represents an epitope of the HIV Tat protein.  
XX The invention relates to a composition containing a peptide of formulae  
CC (I)-(IV): R1-VP-y-LEP-R2 (I); R3-K-x-IGISYGRK-R4 (II);  
CC R5-RR-x'zay'-S-R6 (III); R7-SQ-x''-HQ-y''-SHSKOP-R8 (IV); where:  
CC y = R, K, S, N or ornithine; R1, R3, R5 and R7 = hydrogen, lower alkyl or  
CC alkanoyl, or 1-5 (for R1 and R3) or 1-3 (for R5 and R7) amino acids (aa),  
CC optionally substituted by lower alkyl or alkanoyl; R2 = free hydroxy,  
CC amide or 1-14 additional aa, optionally substituted by lower alkyl or  
CC alkanoyl; x = G or A; R4 = hydroxy, amide or 1-5 additional aa,  
CC optionally substituted by amide; x' = A, P, S or Q; y' = D, N, G or S;  
CC z = P or H; a = Q or P; R6 = hydroxy or amide; x'' = N or T;  
CC y'' = A or V, and R8 = hydroxy, amide or 1-3 additional aa, optionally  
CC substituted by amide. The compositions, and synthetic molecules, viruses,  
CC or bacteria containing them, are used to induce Ab that react with over  
CC 95, best 99, % of known human immunodeficiency virus (HIV)-1 Tat  
CC proteins, particularly to reduce HIV-1 levels in both infected and  
CC uninfected subjects (provided they are still immunocompetent). Antibodies  
CC (Ab) against the peptides reduce viral multiplication during initial  
CC infection and minimise the chronic viraemia that leads to acquired immune  
CC deficiency syndrome. Ab are used to reduce HIV-1 levels in infected  
CC subjects unable to mount an immune response (passive immunisation).  
CC Peptides (I)-(IV) represent four different epitopes in Tat protein and a  
CC relatively small number of them will induce antibodies cross-reactive  
CC with most strains and variants of Tat. The content of the composition is  
CC easily adjusted to account for and new strains discovered. They can be  
CC administered in the early stages of, or before, infection and do not  
CC promote selection of escape mutants.

SO Sequence 7 AA;

Query Match 18.2%; Score 4; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 PKLE 21  
|||  
Db 3 PKLE 6

RESULT 10

AAB87883  
ID AAB87883 standard; peptide: 7 AA.

AAB87883;

17-MAY-2001 (first entry)

Epitope I peptide #2.

Tat; HIV-1; human immunodeficiency virus; AIDS; viraemia.

Unidentified.

US6193981-B1.

27-FEB-2001.

10-JUL-1998; 98US-0113921.

11-JUL-1997; 97US-0893853.

(THYM-) THYMON LLC.

Goldstein G;

XX  
DR WPI: 2001-243400/25.  
XX  
PT New compositions comprising at least two variants of a Tat protein  
PT coupled to a carrier protein, useful for impairing multiplication of  
PT human immunodeficiency virus 1 and in eliciting anti-TAT antibodies  
XX  
PS Claim 4; Column 9; 63pp; English.  
XX  
CC The present invention relates to a composition with at least two  
CC variants of Tat protein coupled to a carrier protein. The invention is  
CC useful for inhibiting the multiplication of HIV-1 virus in infected  
CC patients with viremia, symptomatic or asymptomatic and for  
CC attenuating HIV-1 multiplication during primary infection in  
CC previously uninfected subjects.  
XX  
SQ Sequence 7 AA;

Query Match 18.2%; Score 4; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

OY 18 PKLE 21  
||||  
Db 3 pkle 6

RESULT 11  
AAR73549  
ID AAR73549 standard; Peptide: 8 AA.  
XX  
AC AAR73549;  
XX  
DT 19-DEC-1995 (first entry)  
XX  
DE Human TSH receptor (residues 697-704).  
XX  
KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens;  
KW antibody; affinity; detection.  
XX  
OS Synthetic.  
XX  
PN JP07089991-A.  
XX  
PD 04-APR-1995.  
XX  
PF 28-SEP-1993; 93JP-0240853.  
XX  
PR 28-SEP-1993; 93JP-0240853.  
XX  
PA (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.  
XX  
DR WPI: 1995-167251/22.  
XX  
PT Novel polypeptide(s) having affinity for the human TSH receptor  
PT antibody - used in detection of the TSH antibody.  
XX  
PS Claim 1; Page 47; 54pp; Japanese.  
XX  
CC Peptides with affinity to human TSH (thyroid stimulating hormone)  
CC receptor antibody are used for detection of the antibody. (See also  
CC AAR73201-592).  
XX  
SQ Sequence 8 AA;

Query Match 18.2%; Score 4; DB 16; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;  
OY 4 ROAQ 7  
||||

Db 5 rqaq 8

RESULT 12  
AAR73551  
ID AAR73551 standard; Peptide: 8 AA.  
XX  
AC AAR73551;  
XX  
DT 19-DEC-1995 (first entry)  
XX  
DE Human TSH receptor (residues 701-708).  
XX  
KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens;  
KW antibody; affinity; detection.  
XX  
OS Synthetic.  
XX  
PN JP07089991-A.  
XX  
PD 04-APR-1995.  
XX  
PF 28-SEP-1993; 93JP-0240853.  
XX  
PR 28-SEP-1993; 93JP-0240853.  
XX  
PA (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.  
XX  
DR WPI: 1995-167251/22.  
XX  
PT Novel polypeptide(s) having affinity for the human TSH receptor  
PT antibody - used in detection of the TSH antibody.  
XX  
PS Claim 1; Page 48; 54pp; Japanese.  
XX  
CC Peptides with affinity to human TSH (thyroid stimulating hormone)  
CC receptor antibody are used for detection of the antibody. (See also  
CC AAR73201-592).  
XX  
SQ Sequence 8 AA;

Query Match 18.2%; Score 4; DB 16; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

OY 4 ROAQ 7  
||||  
Db 1 rqaq 4

RESULT 13  
AAW59591  
ID AAW59591 standard; peptide: 8 AA.  
XX  
AC AAW59591;  
XX  
DT 23-OCT-1998 (first entry)  
XX  
DE Epitope of the Hepatitis C virus.  
XX  
KW Epitope; HCV; envelope protein E2; HCV antibody; anti-1dotype;  
KW vaccine; HCV infection; treatment; diagnosis.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
PN W09816647-A1.  
XX  
PD 23-APR-1998.  
XX  
PF 03-OCT-1997; 97WO-JP03551.  
XX

PR 03-MAR-1997; 97JP-0065448.  
 PR 14-OCT-1996; 96JP-0293359.  
 XX  
 PA (KAGA ) CHERO-SERO-THERAPEUTIC RES INST.  
 XX  
 PI Makizumi K, Mizuno K, Nishihara T, Nishimura S;  
 PI Nozaki C, Rikihisa T;  
 XX  
 DR WPI; 1998-261043/23.  
 XX  
 PT Hepatitis C virus envelope antigen epitope peptide(s) - useful for,  
 PT e.g. treatment, vaccination and detection of hepatitis C virus  
 PT infection(s)  
 PS  
 XX Disclosure; Fig 14; 99pp; Japanese.  
 CC  
 CC AAM59504-608 represent epitopes of the Hepatitis C virus (HCV). The  
 CC peptides are derived from the HCV envelope protein E2 (384-414 region)  
 CC and are capable of binding to HCV antibodies. The epitope peptides and  
 CC anti-idiotypic antibodies can be used to produce effective vaccines  
 CC against HCV infection. The antibodies recognising the epitope peptides  
 CC can be used in the treatment of HCV infection. The epitope peptides,  
 CC DNA and antibodies can be used for diagnosis of HCV infection, detection  
 CC of the presence of HCV and for HCV neutralising antibody assay.  
 CC  
 SQ Sequence 8 AA;

Query Match 18.2%; Score 4; DB 19; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ODIO 10  
 IIII  
 Db 3 qdiq 6

RESULT 14  
 AAR37604  
 ID AAR37604 standard; peptide; 9 AA.  
 XX  
 AC AAR37604;  
 XX  
 DT 13-OCT-1993 (first entry)  
 XX  
 DE hIL2R Ab L chain V region CDR3.  
 XX  
 KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;  
 KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;  
 KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;  
 KW region; PCR; framework; plasmid.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9311238-A.  
 XX  
 PD 10-JUN-1993.  
 XX  
 PF 03-DEC-1992; 92WO-JP01583.  
 XX  
 PR 06-DEC-1991; 91JP-0323319.  
 XX  
 PA (BIOT ) BIOTEST PHARMA GMBH.  
 PA (INNO-) INNOTHERAPIE LAB.  
 PA (SUMU ) SUMITOMO PHARM CO LTD.  
 XX  
 PI Gomi H, Nakatani T, Noguchi H, Wajdenes J;  
 XX  
 DR WPI; 1993-197057/24.  
 XX  
 PT Humanised antibody comprising - CDR region of mouse MAB B-B10  
 PT specific for IL-2 receptor useful for treating carcinoma  
 PT expressing IL-2 receptor

XX  
 PS Claim 1; Page 43; 62pp; English.  
 XX  
 CC The sequences given in AAR37599-604 represent the complementarity-  
 CC determining regions (CDRs) of a humanised antibody (Ab) which binds  
 CC specifically to human interleukin (IL)-2 receptor (hIL2R). These  
 CC CDRs were derived from the murine anti-human IL-2 receptor monoclonal  
 CC Ab (Mab) B-B10 (see also AA043242-43). This Mab is antagonistic to the  
 CC binding of IL-2 to the IL-2 receptor on human T-cells. It also  
 CC inhibits the human mixed lymphocyte reaction. The cDNA encoding the  
 CC variable (V) region of the B-B10 Ab was cloned by PCR and sequenced  
 CC (see also AA043226-32 and AA043233-36). A human Ab with high levels of  
 CC amino acid sequence homology to the murine sequence was selected and  
 CC the framework of this Ab was bound with the B-B10 V region CDR and a  
 CC part of the framework to design several kinds of the humanised B-B10 V  
 CC region (see also AA043244-45). The DNA sequence coding this humanised  
 CC B-B10 was synthesised and a plasmid expressing humanised B-B10 was  
 CC constructed.  
 CC  
 SQ Sequence 9 AA;

Query Match 18.2%; Score 4; DB 14; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 SSWP 18  
 IIII  
 Db 4 sswp 7

RESULT 15  
 AAR42576  
 ID AAR42576 standard; peptide; 9 AA.  
 XX  
 AC AAR42576;  
 XX  
 DT 28-JUL-1994 (first entry)  
 XX  
 DE HLA epitope.  
 XX  
 KW Epitope; immuno-homologue; HLA; heavy chain; alpha-1 domain; allele;  
 KW cW4; superantigen; immunodiagnostic; AIDS; HIV; immunisation;  
 KW vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9323427-A.  
 XX  
 PD 25-NOV-1993.  
 XX  
 PF 10-MAY-1993; 93WO-IT00049.  
 XX  
 PR 11-MAY-1992; 92IT-0RM0350.  
 XX  
 PA (SANR-) FOND CENT SAN ROMANELLO DEL MONTE TABOR.  
 PA (SUPE-) INST SUPERIORE DI SANITA.  
 XX  
 PI Beretta A;  
 XX  
 DR WPI; 1993-386478/48.  
 XX  
 PT HIV gp160 epitope(s) immunologically homologous to HLA - used to  
 PT develop agents for immuno-diagnosis and vaccines for HIV  
 PT infection  
 XX  
 PS Claim 9; Page 14; 31pp; English.  
 CC  
 CC The patent claims epitopes of the HIV gp160 protein which are  
 CC immunologically homologous to at least one epitope of the HLA  
 CC protein family, preferably the HLA class I protein heavy chains.  
 CC The present sequence is a region of the heavy chain alpha-1 domain,  
 CC cW4 allele, to which the epitopes are homologous.

CC The identification of HIV gp160 epitopes homologous to HLA epitopes  
CC can be used to develop agents for vaccines and immunodiagnosis of  
CC HIV infection. The HIV homologous HLA regions are able to induce  
CC anti-HLA autoantibodies and act as superantigens during the  
CC infection course, leading to a gradual and selective loss of  
CC certain T receptor families.

XX  
SQ Sequence 9 AA;

Query Match 18.2%; Score 4; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RQAG 7  
| | | |  
DB 6 rgaq 9

Search completed: July 23, 2001, 16:56:13  
Job time: 530 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 17:06:06 ; Search time 69.82 Seconds  
(without alignments)  
41.689 Million cell updates/sec

Title: US-09-351-296-14  
Perfect score: 22  
Sequence: 1 QASKQADIQPAVQASWPKVEQ 22

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5654

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

SPREMBL\_16:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	6	27.3	18	09X3N3	09X3N3 neisseria m
2	4	18.2	18	09S8G8	09S8G8 psobocarpu
3	4	18.2	20	09R509	09R509 bacillus al
4	4	18.2	20	09S947	09S947 saccharomyc
5	4	18.2	21	10	041566 triticum ae
6	4	18.2	22	13	09PRY6
7	3	13.6	8	5	094695 physarum po
8	3	13.6	9	2	P70740
9	3	13.6	10	2	09X8N3
10	3	13.6	10	2	09F9H5
11	3	13.6	11	2	09R446
12	3	13.6	11	2	09K332
13	3	13.6	11	5	023876
14	3	13.6	11	5	09TRX6
15	3	13.6	11	5	09NFX0
16	3	13.6	11	11	062207
17	3	13.6	12	2	052112
18	3	13.6	12	4	09UC37
19	3	13.6	12	4	09H3W2

20	3	13.6	12	8	031851	031851 arabidopsis
21	3	13.6	12	13	09PVC7	09PVC7 esox lucius
22	3	13.6	12	13	09PVC6	09PVC6 pleoclossu
23	3	13.6	12	13	09PVC4	09PVC4 harpadon sp
24	3	13.6	12	13	09PVC3	09PVC3 lampiris sp.
25	3	13.6	12	13	09PVC2	09PVC2 gadus morhu
26	3	13.6	12	13	09PVC1	09PVC1 lophius sp.
27	3	13.6	12	13	09PVC0	09PVC0 mugil japon
28	3	13.6	12	13	09PVB9	09PVB9 oryzias lat
29	3	13.6	12	13	09PVB8	09PVB8 hemiramphus
30	3	13.6	12	13	09PVA8	09PVA8 mulius sp.
31	3	13.6	13	2	050038	050038 mycobacteri
32	3	13.6	13	2	031295	031295 buchnera ap
33	3	13.6	13	2	09R2P8	09R2P8 escherichia
34	3	13.6	13	2	P82560	P82560 streptococc
35	3	13.6	13	4	09Y674	09Y674 homo sapien
36	3	13.6	13	8	09T569	09T569 zeia mayis (m
37	3	13.6	13	10	09S941	09S941 beta vulgar
38	3	13.6	13	13	09PVC5	09PVC5 galaxias ma
39	3	13.6	13	13	09PVB7	09PVB7 fundulus be
40	3	13.6	13	13	09PVB6	09PVB6 poecilia la
41	3	13.6	13	13	09PVB5	09PVB5 sarcocentro
42	3	13.6	13	13	09PVB4	09PVB4 zeus faber
43	3	13.6	13	13	09PVB3	09PVB3 hippocampus
44	3	13.6	13	13	09PVB2	09PVB2 mastacembel
45	3	13.6	13	13	09PVB1	09PVB1 dendrochiru

#### ALIGNMENTS

RESULT 1  
ID 09X3N3 PRELIMINARY; PRT: 18 AA.  
AC 09X3N3;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE HYPOTHEMETICAL 1.9 KDA PROTEIN.  
GN REP2.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_Taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58;  
RX MEDLINE=97089756; PubMed=8935664;  
RA Peak I.R., Jennings M.P., Hood D.W., Bisceric M., Moxon E.R.;  
RT "tetranucleotide repeats identify novel virulence determinant  
variation in Haemophilus also occur in Neisseria spp. and Moraxella  
catarrhalis.";  
RL FEWS Microbiol. Lett. 137:109-114(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58;  
RX MEDLINE=99141213; PubMed=9973577;  
RA Peak I.R., Jennings M.P., Hood D.W., Moxon E.R.;  
RT "tetranucleotide repeats identify novel virulence determinant  
in Neisseria meningitidis.";  
RL Microb. Pathog. 26:13-23(1999).  
DR EMBL: AF073778; AAD24876.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 18 AA: 1907 MW: 7FD2943EC4329B2A CRC64;

Query Match 27.3%; Score 6; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QASKOA 6  
Db 8 QASKOA 13

```

RESULT 2
ID 09S8G8 PRELIMINARY: PRT: 18 AA.
AC 09S8G8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE PROLINE-RICH PROTEIN (FRAGMENT).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
CC Fabales; Fabaceae; Papilionoideae; Psophocarpus.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=95277008; PubMed=7757337;
RA Esaka M., Hayakawa H.;
RT "Specific secretion of proline-rich proteins by salt-adapted winged
RT bean cells."
RL Plant Cell Physiol. 36:441-446(1995).
SQ SEQUENCE 18 AA: 2252 MW: 4FD7D1DA18B5D94A CRC64;

Query Match 18.2%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PKVE 21
DB 9 PKVE 12

RESULT 3
ID 09R509 PRELIMINARY: PRT: 20 AA.
AC 09R509;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE ADENYLATE KINASE (EC 2.7.4.3) (FRAGMENT).
OS Bacillus alcalophilus.
CC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus.
OX NCBI_TaxID=1445;
RN [1]
RP SEQUENCE.
RX MEDLINE=94117390; PubMed=8288548;
RA Gilles A.M., Glaser P., Perrier V., Meler A., Longin R., Sebald M.,
RA Maiguen L., Pistotnik E., Barzu O.;
RT "Zinc, a structural component of adenylate kinases from gram-positive
RT bacteria."
RL J. Bacteriol. 176:520-523(1994).
DR InterPro: IPR000850; -;
DR Pfam: PF00406; adenylatekinase: 1.
SQ SEQUENCE 20 AA: 2190 MW: 94D98FC289220254 CRC64;

Query Match 18.2%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PKVE 21
DB 9 PKVE 12

RESULT 4
ID 09S947 PRELIMINARY: PRT: 20 AA.
AC 09S947;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

```

```

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MITOCHONDRIAL CYTOCHROME OXIDASE SUBUNIT I (EC 1.9.3.1) (FRAGMENT).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Mitochondrion.
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Novitski C.E., Macreadie I.G., Maxwell R.J., Lukins H.B.,
RA Linnane A.W., Nagley P.;
RL Curr. Genet. 8:135-146(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85035872; PubMed=6387398;
RA Simon M., Faye G.;
RT "Organization and processing of the mitochondrial ox13/ol12 multigenic
RT transcript in yeast."
RL Mol. Gen. Genet. 196:266-274(1984).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: M36379; AAA32147.1; -;
DR EMBL: X00960; CAA25472.1; -;
KW Mitochondrion; Oxidoreductase; Heme; Copper; Transmembrane;
KW Respiratory chain.
FT NON_TER 1
SQ SEQUENCE 20 AA: 2142 MW: A4F7B024CD94F2D6 CRC64;

```

```

Query Match 18.2%; Score 4; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PAVQ 14
DB 16 PAVQ 19

RESULT 5
ID 041566 PRELIMINARY: PRT: 21 AA.
AC 041566;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HEAT SHOCK PROTEIN 16.9 (FRAGMENT).
GN HSP16.9-1LCL.
OS Triticum aestivum (Wheat).
CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
CC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae;
CC Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MUSTANG;
RA Joshi C.P., Nguyen H.T.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: L37071; AAA51391.1; -;
KW Heat shock.
FT NON_TER 1
SQ SEQUENCE 21 AA: 2248 MW: 522524E70B3320F4 CRC64;

```

```

Query Match 18.2%; Score 4; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PKVE 21
DB 5 PKVE 8

```



RESULT 6  
Q9PRV6 PRELIMINARY: PRT: 22 AA.  
AC Q9PRV6  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE TCDD-ARACHIDONIC ACID EPOXYGENASE (FRAGMENT).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94148833; PubMed=8106378;  
RA Rifkind A.B., Kaneoshi A., Orlickick J., Capdevilla J.H., Lee C.;  
RT "Purification and biochemical characterization of two major cytochrome  
RT P-450 isoforms induced by 2,3,7,8-tetrachlorodibenzo-p-dioxin in chick  
RT embryo liver.";  
RL J. Biol. Chem. 269:3387-3396(1994).  
SO SEQUENCE 22 AA: 2246 MW: 121CA7298A2646B6 CRC64;

Query Match 18.2%; Score 4; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VOAS 16  
Db 8 VOAS 11

RESULT 7  
Q94695 PRELIMINARY: PRT: 8 AA.  
AC Q94695  
DT 01-FEB-1997 (TREMBlrel. 02, Created)  
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE ACTIN (FRAGMENT).  
GN ARDC.  
OS Physarum polycephalum (Slime mold).  
OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;  
OC Physarum.  
OX NCBI\_TaxID=5791;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96182101; PubMed=8622700;  
RA Benard M., Lagneel C., Pallotta D., Pierron G.;  
RT "Mapping of a replication origin within the promoter region of two  
RT unlinked, abundantly transcribed actin genes of Physarum  
RT polycephalum.";  
RL Mol. Cell. Biol. 16:968-976(1996).  
DR EMBL: M73459; AAB03706.1; -;  
FT NON\_TER 8  
SO SEQUENCE 8 AA: 878 MW: F4C6C2CAAB187B16 CRC64;

Query Match 13.6%; Score 3; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VOA 15  
Db 6 VOA 8

RESULT 8  
P70740 PRELIMINARY: PRT: 9 AA.  
AC P70740;

DT 01-FEB-1997 (TREMBlrel. 02, Created)  
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE HOXX, HOXA AND HYPE GENES (FRAGMENT).  
GN HOXA.  
OS Alcaligenes eutrophus (Ralstonia eutropha).  
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;  
OC Ralstonia.  
OX NCBI\_TaxID=510;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H16;  
RX MEDLINE=94292469; PubMed=8021224;  
RA Lenz O., Schwartz E., Derredde J., Eitinger M., Friedrich B.;  
RT "The Alcaligenes eutrophus H16 hoxx gene participates in hydrogenase  
RT regulation.";  
RL J. Bacteriol. 176:4385-4393(1994).  
DR EMBL: X74670; CAA52736.1; -;  
FT NON\_TER 9  
SO SEQUENCE 9 AA: 992 MW: 970BD1ADC6D33AB5 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KOA 6  
Db 4 KOA 6

RESULT 9  
Q9XBH3 PRELIMINARY: PRT: 10 AA.  
AC Q9XBH3  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE CELF-LIKE PROTEIN (FRAGMENT).  
GN CELF.  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=1396;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 10987;  
RX MEDLINE=99231848; PubMed=10217496;  
RA Ostad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;  
RT "Genome organization is not conserved between Bacillus cereus and  
RT Bacillus subtilis.";  
RL Microbiology 145:621-631(1999).  
DR EMBL: AJ000394; CAB40625.1; -;  
FT NON\_TER 1  
SO SEQUENCE 10 AA: 1264 MW: D3757EC3339C9D6 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 KVE 21  
Db 7 KVE 9

RESULT 10  
Q9F9H5 PRELIMINARY: PRT: 10 AA.  
AC Q9F9H5;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE GLUTAMATE RACEMASE (FRAGMENT).  
 GN GLR.  
 OC Helicobacter pylori (campylobacter pylori).  
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
 OC Helicobacter.  
 OX NCBI\_TaxID=210;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-INDIA75A;  
 RX MEDLINE=20270132; PubMed=10809702;  
 RA Kersulyte D., Mukhopadhyay A.K., Velapattin B., Su W.W., Pan Z.J.,  
 RA Garcia C., Hernandez V., Valdez Y., Mistry R.S., Gilman R.H., Yuan Y.,  
 RA Gao H., Alarcon T., Lopez-Brea M., Balakrish Nair G., Chowdhury A.,  
 RA Datta S., Shital F.O., Nakazawa T., Ally R., Segal I., Wong B.C.,  
 RA Lam S.K., Olfat F.O., Boren T., Engstrand L., Torres O., Schneider R.,  
 RA Thomas J.E., Czinn S., Berg D.E.;  
 RT "Differences in genotypes of Helicobacter pylori from different human  
 populations.";  
 RT J. Bacteriol. 182:3210-3218(2000).  
 RL EMBL: AF190663; AAG18486.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA: 1273 MW: CAD126337B133DC6 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 KOA 6  
 Db 2 KOA 4

RESULT 11  
 ID 09R446 PRELIMINARY; PRT; 11 AA.  
 AC 09R446;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE CARBAMOYL-PHOSPHATE SYNTHASE SUBUNIT A (FRAGMENT).  
 GN CARA.  
 OS Neisseria gonorrhoeae.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=485;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MS11, AND FA1090;  
 RX MEDLINE=95291461; PubMed=7773412;  
 RA Lawson F.S., Billowes F.M., Dillon J.A.;  
 RT "Organization of carbamoyl-phosphate synthase genes in Neisseria  
 gonorrhoeae includes a large, variable intergenic sequence which is  
 also present in other Neisseria species.";  
 RT Microbiology 141:0-0(0).  
 RL [2]  
 RN RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MS11, AND FA1090;  
 RA Brinkman F.S.L., Francis F.M., Dillon J.R.;  
 RT "Complexity of the variable sequence between the carbamoyl-phosphate  
 synthase genes of Neisseria species.";  
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AF029363; AAC78453.1; -.  
 DR EMBL: AF029362; AAC78452.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 11 AA: 1178 MW: 0C07A8E3DD33694 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 KOA 6  
 Db 2 KOA 4

Db 9 KOA 11

RESULT 12  
 ID 09K332 PRELIMINARY; PRT; 11 AA.  
 AC 09K332;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE GH (FRAGMENT).  
 GN GH.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VARIOUS STRAINS;  
 RX MEDLINE=20187516; PubMed=10722640;  
 RA Cramton S.E., Schnell N.F., Goltz F., Bruckner R.;  
 RT "Identification of a new repetitive element in Staphylococcus  
 aureus.";  
 RT Infect. Immun. 68:2344-2348(2000).  
 RL EMBL: AF195967; AAF60251.1; -.  
 DR EMBL: AF195963; AAF60243.1; -.  
 DR EMBL: AF195964; AAF60245.1; -.  
 DR EMBL: AF195965; AAF60247.1; -.  
 DR EMBL: AF195966; AAF60249.1; -.  
 DR InterPro: IPR001189; -.  
 DR ProDom: PD000475; -; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 11 AA: 1262 MW: 4F978F86AAB1A723 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 KOA 6  
 Db 9 KOA 11

RESULT 13  
 ID 023876 PRELIMINARY; PRT; 11 AA.  
 AC 023876;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE ACTIN 4.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82260445; PubMed=6286214;  
 RA Mckeown M., Firtel R.A.;  
 RT "Actin multigene family of Dictyostelium.";  
 RT Cold Spring Hard. Symp. Quant. Biol. 46:495-505(1982).  
 RL EMBL: K02957; AAA33150.1; -.  
 DR EMBL: K02956; AAA33150.1; JOINED.  
 SQ SEQUENCE 11 AA: 1205 MW: 728B4C14C6C2CAAB CRC64;

Query Match 13.6%; Score 3; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 13 KOA 15  
 Db 6 KOA 8

Search completed: July 23, 2001, 17:06:06  
 Job time: 547 sec

## RESULT 14

O9Twx6 PRELIMINARY: PRT: 11 AA.  
 AC O9Twx6;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
 DE JUVENILE HORMONE BINDING PROTEIN. JHBP-12.5 KDA CNBR PEPTIDE.  
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Sphingioidea; Sphingidae; Sphinginae; Manduca.  
 OX NCBI\_TaxID=7130;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92134256; PubMed=1734862;  
 RA Touhara K., Prestwich G.D.;  
 RT "Binding site mapping of a photoaffinity-labeled juvenile hormone  
 binding protein."  
 RL Biochem. Biophys. Res. Commun. 182:466-473(1992).  
 SO SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;

## Query Match

Best Local Similarity 13.6%; Score 3; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QAS 3  
 |||

Db 3 QAS 5

## RESULT 15

Q9NFX0

ID Q9NFX0 PRELIMINARY: PRT: 11 AA.  
 AC Q9NFX0;

DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE MITOCHONDRIAL ACONITASE (FRAGMENT).

OS ACON OR MAC OR CG9244.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;  
 [1]

RN SEQUENCE FROM N.A.  
 RP STRAIN-CANTON S;

RC LIND M.I.;

RT "Characterisation of two iron regulatory proteins and mitochondrial  
 aconitase in Drosophila melanogaster."

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

EMBL: AJ252019; CAB93522.1; -

DR FLYBase; FBgn0010100; Acon.

DR InterPro; IPR01886; -

DR PRODom; PD002082; -; 1.

DR NON\_TER 11

FT 11

SO SEQUENCE 11 AA; 1204 MW; 7C889CEAD4469734 CRC64;

## Query Match

Best Local Similarity 13.6%; Score 3; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 QAO 7  
 |||

Db 9 QAO 11

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 17:04:49 ; Search time 23.18 Seconds  
(without alignments)  
32.512 Million cell updates/sec

Title: US-09-351-296-14

Perfect score: 22

Sequence: 1 QASKQADIDIPAVQASMPKVEQ 22

Scoring table:

OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1176

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database: SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	18.2	13	ACT7_SOYBN	P15987 glycine max
2	4	18.2	15	PGKH_PHYPA	P80659 physcomltre
3	4	18.2	17	ACT6_SOYBN	P15986 glycine max
4	4	18.2	21	FEDB_AWME	P80706 amycolatops
5	3	13.6	7	LANC_CARUT	P36960 carnobacter
6	3	13.6	9	ULAH_HUMAN	P31934 homo sapien
7	3	13.6	10	BPP_VIPAS	P31351 vipera aspi
8	3	13.6	10	COXA_ONCMY	P80328 oncorhynch
9	3	13.6	10	CAJU_HUMAN	P30358 homo sapien
10	3	13.6	10	UPA5_HUMAN	P30091 homo sapien
11	3	13.6	10	UPA8_HUMAN	P30094 homo sapien
12	3	13.6	10	UXA2_CHLTR	P38003 chlamydia t
13	3	13.6	13	IDHP_RAT	P56574 rattus norv
14	3	13.6	15	PDGB_PIG	P20034 sus scrofa
15	3	13.6	17	JHBP_PLAVG	P56675 platyprepia
16	3	13.6	17	NEF_HV1J3	P12480 human immun
17	3	13.6	18	AL13_CARMA	P81816 carcinus ma
18	3	13.6	18	DRPH_UCAPL	P08871 uca pugilat
19	3	13.6	18	FIBB_ANAPL	P12802 anas platyr
20	3	13.6	19	ADC_CLOPA	P81336 clostridium
21	3	13.6	19	FIBB_PIG	P14477 sus scrofa
22	3	13.6	19	RL10_CITFR	P33448 citrobacter
23	3	13.6	20	ALBG_EQUAS	P39090 equus asinu
24	3	13.6	20	CD4_SHEEP	P05542 ovis aries
25	3	13.6	20	COG1_PARC	P80721 parathiodo
26	3	13.6	20	COXA_THOUB	P80972 thunnus obe
27	3	13.6	20	CUDP_VERCH	P80406 verticilliu
28	3	13.6	20	DER6_DERPT	P49277 dermatophag
29	3	13.6	20	ELAS_GADMO	P32197 gadus morhu
30	3	13.6	20	OMPI_ACTAC	P20242 actinobacil
31	3	13.6	20	PSAF_PEA	P20119 pisum sativ
32	3	13.6	20	RL10_PROVU	P51411 proteus vul
33	3	13.6	20	SODM_HORVU	P28524 hordeum vul

34	3	13.6	20	1	VR90 BORPE	P81549 boordetella
35	3	13.6	21	1	FIBB_BISBO	P14466 bison bonas
36	3	13.6	21	1	GYRA_STRSH	P50071 streptomyc
37	3	13.6	21	1	NKLA_ACISP	P33036 actinobact
38	3	13.6	21	1	PSAL_SYPN6	P31084 synechococc
39	3	13.6	21	1	SRTD_ATREN6	P13211 atractaspis
40	3	13.6	22	1	MOTI_CHICK	O99P6 gallus gall
41	3	13.6	22	1	RL10_CHEPN	P41190 klebsiella
42	2	9.1	6	1	LOK1_LOCHI	P41491 locusta mig
43	2	9.1	7	1	CIA_ENTFA	P11932 enterococcu
44	2	9.1	7	1	UF04_MOUSE	P38642 mus musculi
45	2	9.1	7	1	UH11_RAT	P56576 rattus norv

## ALIGNMENTS

```

RESULT 1
ACT7_SOYBN
ID ACT7_SOYBN STANDARD; PRT; 13 AA.
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ACTIN 7 (FRAGMENT).
GN SACT7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. WAYNE;
RX MEDLINE=91346640; Pubmed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBICUOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -1- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
-----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL: X17120; CAA34980.1; -
CC PIR: S15755; S15755.
CC InterPro: IPR000279; -
DR PROSITE: PS00406; ACTINS_1; PARTIAL.
DR PROSITE: PS00432; ACTINS_2; PARTIAL.
DR PROSITE: PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON_TER 13
SQ
SEQUENCE 13 AA; 1420 MW; 8BEEF3C36D4FD05A CRC64;

```

Query Match 18.2%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 DIOP 11  
 ||||  
 DB 6 DIOP 9

## RESULT 2

PGKH\_PHYPA STANDARD: PRT; 15 AA.  
 ID PGKH\_PHYPA STANDARD: PRT; 15 AA.  
 AC P80659;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE PHOSPHOGLYCERATE KINASE, CHLOROPLAST (FRAGMENT).  
 OS Physcomitrella patens (Moss).  
 CC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;  
 CC Funariidae; Funariales; Funariaceae; Physcomitrella.  
 CC NCBI\_TaxID=3218;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Protonema;  
 RX MEDLINE=97275459; PubMed=9129336;  
 RA Kasten B., Buck F., Nuske J., Reski R.;  
 RT "Cytoxinin affects nuclear- and plastome-encoded energy-converting  
 RL plastid enzymes.";  
 RL Planta 201:261-272(1997).  
 CC -1- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP +  
 CC 3-PHOSPHO-D-GLYCEROL, PHOSPHATE.  
 CC -1- PATHWAY: CALVIN CYCLE.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.  
 DR InterPro: IPR001576; -  
 DR PROSITE: PS00111; PGlycerate kinase; PARTIAL.  
 DR Transferrase; Kinase; Multigene family; Calvin cycle; Chloroplast.  
 KW NON\_TER 15  
 FT SEQUENCE 15 AA; 1531 MW; 56A5EC1F677EEC6 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QASK 4  
 ||||  
 DB 5 QASK 8

RESULT 3  
 ACT6\_SOYBN STANDARD: PRT; 17 AA.  
 ID ACT6\_SOYBN STANDARD: PRT; 17 AA.  
 AC P15986;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ACTIN 6 (FRAGMENT).  
 GN SAG6.  
 OS Glycine max (Soybean).  
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
 CC Fabales; Fabaceae; Papilionoideae; Glycine.  
 CC NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. MAYNE;  
 RX MEDLINE=91346640; PubMed=2102831;  
 RA Pearson L., Meagher R.B.;  
 RT "Diverse soybean actin transcripts contain a large intron in the 5'  
 RT untranslated leader: structural similarity to vertebrate muscle actin  
 RT genes.";  
 RL Plant Mol. Biol. 14:513-526(1990).  
 CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
 CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED  
 CC IN ALL EUKARYOTIC CELLS.

Query Match 18.2%; Score 4; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC -1- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN  
 CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,  
 CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.  
 CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL: X17119; CA34979.1; -  
 DR PIR: S15754; S15754.  
 DR InterPro: IPR000279; -  
 DR PROSITE: PS00406; ACTINS\_1; PARTIAL.  
 DR PROSITE: PS00432; ACTINS\_2; PARTIAL.  
 DR PROSITE: PS01132; ACTINS\_ACT LIKE; PARTIAL.  
 KW Structural protein; Multigene family.  
 FT NON\_TER 17  
 FT SEQUENCE 17 AA; 1749 MW; 38E4970D4BEFF3C3 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 DIOP 11  
 ||||  
 DB 6 DIOP 9

RESULT 4  
 FEDB\_AMEYE STANDARD: PRT; 21 AA.  
 ID FEDB\_AMEYE STANDARD: PRT; 21 AA.  
 AC P80706;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE FORMATE ESTER DEHYDROGENASE, BETA CHAIN (EC 1.2.99.-) (FEDH)  
 DE (FRAGMENT).  
 DE Arch.  
 OS Amycolatopsis methanolica.  
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 CC Actinomycetales; Pseudonocardiales; Pseudonocardiaceae;  
 CC Amycolatopsis.  
 CC NCBI\_TaxID=1814;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=NCIB 11946;  
 RX MEDLINE=96140591; PubMed=8554333;  
 RA Kim S.W., Luykx D.M.A.M., de Vries S., Duine J.A.;  
 RT "A second molybdopteroid aldehyde dehydrogenase from Amycolatopsis  
 RT methanolica NCIB 11946.";  
 RL Arch. Biochem. Biophys. 325:1-7(1996).  
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA AND A GAMMA  
 CC CHAIN.  
 CC Oxidoreductase.  
 KW NON\_TER 21  
 FT SEQUENCE 21 AA; 2208 MW; 193F40E0285A03B0 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 AVQA 15  
 ||||  
 DB 17 AVQA 20

```

RESULT 5
LANC_CARUI
ID LANC_CARUI STANDARD: PRT: 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LANTIBIOTIC CARNOCIN U149 (FRAGMENT).
OS Carnobacterium sp. (strain U149).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stofield G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -1- FUNCTION: LANTHONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
CC ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON_TER 7
SQ SEQUENCE 7 AA: 786 MW; 741776D05B05H810 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 IOP 11
    |||
Db 4 IOP 6

RESULT 6
ULAH_HUMAN
ID ULAH_HUMAN STANDARD: PRT: 9 AA.
AC P31934;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF LIVER TISSUE (SPOT 94) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX TISSUE=Liver;
RX MEDLINE=94147969; PubMed=831870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 12 KDA.
CC SWISS-2DPAGE: P31934; HUMAN.
FT NON_TER 1
FT VARIANT 3 3 A->L.
FT SEQUENCE 9 AA: 990 MW; F1CC7B172AB6DDCA CRC64;

Query Match 13.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AOD 8
    |||
Db 3 AOD 5

```

```

RESULT 7
BPP_VIPAS
ID BPP_VIPAS STANDARD: PRT: 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Vipera aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubridae;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RX MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Vipera aspis aspis.";
RL Int. J. Biochem. 22:767-771(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
KW PIR; A60377; XASNPC.
FT MOD_RES 1
FT SEQUENCE 10 AA: 1062 MW; 3BA827C327686773 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PKV 20
    |||
Db 6 PKV 8

RESULT 8
COXA_ONCMY
ID COXA_ONCMY STANDARD: PRT: 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE VA (EC 1.9.3.1) (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proctanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits vb and vlla
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
CC 4 FERRICCYTOCHROME C.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR; S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 10

```





RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.65, ITS MW IS: 26.5 KDA.  
 FT NON\_TER 10  
 SO SEQUENCE 10 AA: 1019 MW: 49C285C6CAE862C7 CRC64:

Query Match 13.6%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QAS 3  
 |||  
 Db 7 QAS 9

RESULT 13  
 IDHP\_RAT STANDARD; PRT; 13 AA.  
 AC P56574;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE ISOCITRATE DEHYDROGENASE [NADP], MITOCHONDRIAL (EC 1.1.1.42)  
 DE (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC IDH) (IDP) (ICD-M) (FRAGMENT).  
 GN IDH2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN NCBI\_Taxid=10116;  
 RP SEQUENCE.  
 RC STRAIN=WISTAR; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheeler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.;  
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: PLAYS A ROLE IN INTERMEDIARY METABOLISM AND ENERGY PRODUCTION. IT MAY TIGHTLY ASSOCIATE OR INTERACT WITH THE PYRUVATE DEHYDROGENASE COMPLEX (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ISOCITRATE + NADP(+) = 2-OXOGLOUTARATE + CO(2) + NADPH.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN (SPOT P6) IS: 9.0, ITS MW IS: 42 KDA.  
 CC -1- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE DEHYDROGENASES FAMILY.  
 CC Interpro: IPR001804; -  
 DR PROSITE: PS00470: IDH, IMDH, PARTIAL.  
 DR OXALODEDUCTASE; NADP; Glyoxylate bypass; Tricarboxylic acid cycle; KM Mitochondrion.  
 FT NON\_TER 13  
 SO SEQUENCE 13 AA: 1526 MW: 5FB81031723E02C3 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 KVE 21  
 |||  
 Db 6 KVE 8

RESULT 14  
 PDGB\_PIG STANDARD; PRT; 15 AA.  
 AC P20034;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE PLATELET-DERIVED GROWTH FACTOR, B CHAIN (PDGF B-CHAIN) (PDGFB)

DE (FRAGMENT).  
 GN PDGFB.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 RN NCBI\_Taxid=9823;  
 RP SEQUENCE.  
 RX MEDLINE=8512689; Pubmed=6526008;  
 RA Stroobant P., Waterfield M.D.;  
 RT "Purification and properties of porcine platelet-derived growth factor."  
 RT factor.";  
 RL EMBO J. 3:2963-2967(1984).  
 CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.  
 CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN TRANSFORMATION PROCESSES.  
 CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE PDGF RECEPTOR.  
 CC PIR: A22789; A22789.  
 DR Interpro: IPR000072; -  
 DR PROSITE: PS00248; PDGF-1; PARTIAL.  
 DR PROSITE: PS50278; PDGF-2; PARTIAL.  
 DR Mitogen; Growth factor; Proto-oncogene; Platelet.  
 FT NON\_TER 15  
 SO SEQUENCE 15 AA: 1411 MW: DCC39014450251C2 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PAV 13  
 |||  
 Db 5 PAV 7

RESULT 15  
 JHBP\_PLAVG STANDARD; PRT; 17 AA.  
 ID JHBP\_PLAVG  
 AC P56675;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE JUVENILE HORMONE-BINDING PROTEIN (FRAGMENT).  
 GN JHBP.  
 OS Platypreria virginialis (Ranchman's tiger moth).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Noctuoidea; Arctiidae; Platypreria.  
 RN NCBI\_Taxid=30227;  
 RP SEQUENCE.  
 RA Prestwich G.D., Atkinson J.K.;  
 RT "Rapid purification and N-terminal amino acid sequence of a photoaffinity-labeled juvenile hormone binding protein from an arctiid moth larva, Platypreria virginialis."  
 RT Insect Biochem. 20:801-807(1990).  
 RL -1- FUNCTION: PREVENTS JUVENILE HORMONE FROM BEING HYDROLYZED BY GENERAL ESTERASES BY COMBINING WITH IT SPECIFICALLY.  
 CC -1- SUBCELLULAR LOCATION: SECRETED.  
 FT NON\_TER 17  
 SO SEQUENCE 17 AA: 1880 MW: B1205F097732DA8A CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	7	QDI	9
Db	10	QDI	12

Search completed: July 23, 2001, 17:04:50  
Job time: 511 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: July 23, 2001, 16:57:40 ; Search time 41.27 Seconds  
(without alignments)  
40.607 Million cell updates/sec

Title: US-09-351-296-14

Perfect score: 22

Sequence: 1 QASKQADIQPAVQASMPKEVQ 22

Scoring table: OLIGO

Searched: 219241 seqs, 76174552 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4035

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database: PIR\_68:\*

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	18.2	13	2	S15755
2	4	18.2	14	2	S39932
3	4	18.2	17	2	S15754
4	4	18.2	20	2	C44957
5	3	13.6	7	2	P00727
6	3	13.6	7	2	A58718
7	3	13.6	8	2	S70727
8	3	13.6	8	2	P00726
9	3	13.6	8	2	A38887
10	3	13.6	8	2	S45651
11	3	13.6	9	2	PT0326
12	3	13.6	9	2	B46250
13	3	13.6	9	2	PC7073
14	3	13.6	10	1	XASNPC
15	3	13.6	10	2	GXHU1
16	3	13.6	10	2	S43625
17	3	13.6	10	2	S26506
18	3	13.6	10	2	B38887
19	3	13.6	10	2	PH0923
20	3	13.6	11	2	FC4267
21	3	13.6	11	2	P00731
22	3	13.6	11	2	S21727
23	3	13.6	11	2	C38887
24	3	13.6	11	2	I41946
25	3	13.6	12	2	PN0577
26	3	13.6	12	2	PN0578
27	3	13.6	12	2	PN0579
28	3	13.6	12	2	PN0580
29	3	13.6	12	2	PN0581

30	3	13.6	12	2	PN0576	tyrosine 3-monoxy
31	3	13.6	12	2	S43013	hypothetical prote
32	3	13.6	12	2	S27024	Na+/K+-exchanging
33	3	13.6	12	2	S27023	Na+/K+-exchanging
34	3	13.6	12	2	A61503	sterol carrier pro
35	3	13.6	12	2	S51737	T-cell receptor be
36	3	13.6	12	2	S74196	3-hydroxy-3-methyl
37	3	13.6	12	2	A20907	Ig kappa chain J1
38	3	13.6	12	2	H41946	T-cell receptor ga
39	3	13.6	13	2	A26999	carboxylesterase (
40	3	13.6	13	2	A57789	galbladder stone
41	3	13.6	13	2	S52356	hypothetical prote
42	3	13.6	13	2	S23638	Ig kappa chain J s
43	3	13.6	13	2	B61458	Ig kappa chain V-I
44	3	13.6	13	2	A61458	Ig kappa chain V-I
45	3	13.6	13	2	S47388	T-cell antigen rec

## ALIGNMENTS

RESULT 1  
S15755  
actin 7 - soybean (fragment)  
C:Species: Glycine max (soybean)  
C>Date: 20-Feb-1995 #sequence\_revision 29-May-1998 #text\_change 13-Aug-1999  
C:Accession: S15755  
R:Pearson, L.; Meagher, R.B.  
Plant Mol. Biol. 14, 513-526, 1990  
A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untransla  
A:Reference number: S15754; WUID:91346640  
A:Accession: S15755  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-13 <PEAK>  
A:Cross-references: EMBL:X17120; NID:g18527; PIDN:CAA34980.1; PID:g18528  
C:Superfamily: actin  
C:Keywords: cytoskeleton; structural protein

Query Match 18.2%; Score 4; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DIOP 11  
Db 6 DIOP 9

RESULT 2  
S39932  
S-allele-associated glycoprotein S4 - Japanese pear (fragment)  
N:Alternate names: ribonuclease S4  
C:Species: Pyrus serotina (Japanese pear)  
C>Date: 09-Jun-1994 #sequence\_revision 06-Sep-1996 #text\_change 13-Mar-1997  
C:Accession: S39932  
R:Sassa, H.; Hirano, H.; Ikehashi, H.  
Mol. Gen. Genet. 241, 17-25, 1993  
A:Title: Identification and characterization of stylar glycoproteins associated with  
A:Reference number: S39930; WUID:94049676  
A:Accession: S39932  
A:Molecule type: protein  
A:Residues: 1-14 <SMS>  
C:Superfamily: Enterobacter ribonuclease  
C:Keywords: glycoprotein

Query Match 18.2%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 QPAV 13  
IIII

Db 11 QPAV 14

RESULT 3

S15754

actin 6 - soybean (fragment)

C:Species: Glycine max (soybean)

C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 13-Aug-1999

C:Accession: S15754; S08049

R:Pearson, L.; Meagher, R.B.

Plant Mol. Biol. 14, 513-526, 1990

A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated

A:Reference number: S15754; MUID:91346640

A:Accession: S15754

A:Molecule type: DNA

A:Residues: 1-17 <PEA>

A:Cross-references: EMBL:X17119; NID:918525; PIDN:CAA34979.1; PID:918526

A:Superfamily: actin

C:Keywords: cytoskeleton

Query Match 18.2%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 DIOP 11

Db 6 DIOP 9

RESULT 4

C44957

protein L10 - common tobacco (cv. Samsun NN) (fragment)

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 30-Sep-1993

C:Accession: C44957

R:Takeda, S.; Sato, F.; Iida, K.; Yamada, Y.

Plant Cell Physiol. 31, 215-221, 1990

A:Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum

A:Reference number: A44957

A:Accession: C44957

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <TAK>

Query Match 18.2%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 AVQA 15

Db 1 AVQA 4

RESULT 5

P00727

H2 class I protein [imported] - rice (fragment)

C:Species: Oryza sativa (rice)

C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C:Accession: P00727

R:Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension

A:Reference number: P00696

A:Accession: P00727

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <KOM>

Query Match 13.6%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PAV 13

Db 3 PAV 5

RESULT 6

A58718

carnocin U149 - Carnobacterium sp. (fragment)

C:Species: Carnobacterium sp.

C:Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998

C:Accession: A58718

R:Stoffels, G.; Missen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.

Appl. Environ. Microbiol. 58, 1417-1422, 1992

A:Title: Purification and characterization of a new bacteriocin isolated from a Carno

A:Reference number: A58718; MUID:92321768

A:Accession: A58718

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <STO>

C:Keywords: antibiotic; lanthionine

Query Match 13.6%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 IOP 11

Db 4 IOP 6

RESULT 7

S70727

ipgf protein - Shigella flexneri (fragment)

C:Species: Shigella flexneri

C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 08-Oct-1999

C:Accession: S70727

R:Aliaoui, A.; Sansonetti, P.J.; Menard, R.; Barzu, S.; Mounier, J.; Phalipon, A.; Pa

Mol. Microbiol. 17, 461-470, 1995

A:Title: Xig, a membrane protein required for secretion of Shigella spp. Ipa invasion

A:Reference number: S70727; MUID:96100445

A:Accession: S70727

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-8 <ALL>

A:Cross-references: EMBL:Z48957; NID:9929880; PIDN:CAA8821.1; PID:9929881

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995

C:Genetics:

A:Gene: ipgf

Query Match 13.6%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SKQ 5

Db 1 SKQ 3

RESULT 8

P00726

unidentified 4.5/45K [imported] - rice (fragment)

C:Species: Oryza sativa (rice)

C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C:Accession: P00726

R:Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A:Title: A rice protein library; a data-file of rice proteins separated by two-dimens

A:Reference number: P00696

A:Accession: P00726

A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <KOM>

Query Match 13.6%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 AVQ 14  
|||  
Db 1 AVQ 3

RESULT 9  
A38887  
T-cell receptor gamma chain (5L2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C:Accession: A38887  
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene  
A:Reference number: A41946; MID:92049316  
A:Accession: A38887  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-8 <MHE>  
C:Keywords: T-cell receptor

Query Match 13.6%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 ASW 17  
|||  
Db 1 ASW 3

RESULT 10  
S45651  
Probable Na<sup>+</sup>-transporting ATP synthase (EC 3.6.1.-) - Acetobacterium woodii (fragment)  
C:Species: Acetobacterium woodii  
C>Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 07-May-1999  
C:Accession: S45651  
R:Reidlinger, J.; Mueller, V.  
Eur. J. Biochem. 223, 275-283, 1994  
A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as a  
A:Reference number: S45648; MID:94307271  
A:Accession: S45651  
A:Molecule type: protein  
A:Residues: 1-8 <RET>  
A:Experimental source: DSM 1030  
C:Keywords: hydrolase

Query Match 13.6%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASK 4  
|||  
Db 4 ASK 6

RESULT 11  
PT0326  
Ig heavy chain CRD3 region (clone J2-109) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0326  
R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an  
A:Reference number: PT0222; MID:91108337  
A:Accession: PT0326  
A:Molecule type: DNA  
A:Residues: 1-9 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 13.6%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PAV 13  
|||  
Db 3 PAV 5

RESULT 12  
B46250  
alpha-adaptin - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 05-Apr-1995  
C:Accession: B46250  
R:Timmerman, A.P.; Mayrleitner, M.M.; Lukas, T.J.; Chadwick, C.C.; Saito, A.; Watterso  
Proc. Natl. Acad. Sci. U.S.A. 89, 8976-8980, 1992  
A:Title: Inositol polyphosphate receptor and clathrin assembly protein AP-2 are relat  
A:Reference number: A46250; MID:93028388  
A:Accession: B46250  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <TIM>

Query Match 13.6%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PAV 13  
|||  
Db 1 PAV 3

RESULT 13  
PC7073  
ubiquinol--cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: PC7073  
R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y  
Electrophoresis 21, 1853-1871, 2000  
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles o  
A:Reference number: PC7072  
A:Accession: PC7073  
A:Molecule type: protein  
A:Residues: 1-9 <TSU>  
C:Keywords: brain; core protein; oxidoreductase

Query Match 13.6%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PKV 20  
|||  
Db 6 PKV 8

RESULT 14  
XASNPC  
angiotensin-converting enzyme inhibitor - aspic viper  
C:Species: Vipera aspis (aspic viper)

C:/Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 08-Dec-1995  
C:/Accession: A60377  
R:/Komori, Y.; Sugihara, H.  
Int. J. Biochem. 22, 767-771, 1990  
A:/Title: Characterization of a new inhibitor for angiotensin converting enzyme from the  
A:/Reference number: A60377; MUID:90382616  
A:/Accession: A60377  
A:/Molecule type: protein  
A:/Residues: 1-10 <ROM>  
C:/Superfamily: bradykinin-potentiating peptide  
C:/Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid  
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 13.6%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 PKV 20  
|||  
Db 6 PKV 8

## RESULT 15

GXHU1  
gastric juice peptide - human  
C:/Species: Homo sapiens (man)  
C:/Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C:/Accession: A01628  
R:/Heathcote, J.G.; Washington, R.J.  
Int. J. Protein Res. 2, 117-126, 1970  
A:/Title: Peptides of normal human gastric juice.  
A:/Reference number: A01628; MUID:75150968  
A:/Accession: A01628  
A:/Molecule type: protein  
A:/Residues: 1-10 <HEPA>  
A:/Note: a second peptide lacking 1-Leu, but otherwise identical in composition with the  
C:/Superfamily: unassigned animal peptides  
C:/Keywords: stomach

Query Match 13.6%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 KVE 21  
|||  
Db 5 KVE 7

Search completed: July 23, 2001, 16:57:41  
Job time: 283 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:56:52 ; Search time 34.6 Seconds  
(without alignments)  
12.809 Million cell updates/sec

Title: US-09-351-296-14

Perfect score: 22  
Sequence: 1 QASKQADIQPAVQASMPKEVQ 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 193259 seqs, 2014635 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93443

Minimum DB seq length: 6  
Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	2	US-08-845-926-14
2	12	54.5	22	2	US-08-146-028-98
3	12	54.5	22	4	US-08-723-425A-98
4	12	54.5	22	4	US-09-112-206-98
5	8	36.4	22	2	US-08-845-926-15
6	6	27.3	22	2	US-08-146-028-97
7	6	27.3	22	2	US-08-146-028-153
8	6	27.3	22	4	US-08-723-425A-97
9	6	27.3	22	4	US-08-723-425A-153
10	6	27.3	22	4	US-09-112-206-97
11	6	27.3	22	4	US-09-112-206-153
12	5	22.7	22	1	US-08-127-909-11
13	5	22.7	22	1	US-08-127-909-13
14	5	22.7	22	2	US-08-457-353-11
15	5	22.7	22	2	US-08-457-353-13
16	4	18.2	8	2	US-08-616-669A-20
17	4	18.2	8	4	US-09-326-440-20
18	4	18.2	9	3	US-08-159-339A-389
19	4	18.2	10	2	US-08-685-589A-126
20	4	18.2	12	1	US-08-082-844-4
21	4	18.2	12	4	US-08-669-286-18
22	4	18.2	12	4	US-09-469-253-18
23	4	18.2	12	5	PCT-US94-07040-4
24	4	18.2	13	3	US-08-374-077C-47
25	4	18.2	13	3	US-08-374-077C-48
26	4	18.2	13	4	US-08-895-590-89
27	4	18.2	13	4	US-08-895-590-90

28	4	18.2	14	3	US-08-881-094-41	Sequence 41, App1
29	4	18.2	14	4	US-08-602-999A-402	Sequence 402, App
30	4	18.2	15	1	US-08-127-909-6	Sequence 6, App11
31	4	18.2	15	1	US-08-127-909-8	Sequence 8, App11
32	4	18.2	15	2	US-08-457-353-6	Sequence 6, App11
33	4	18.2	15	2	US-08-457-353-8	Sequence 8, App11
34	4	18.2	16	1	US-08-326-117B-20	Sequence 20, App1
35	4	18.2	16	1	US-08-307-724B-5	Sequence 5, App11
36	4	18.2	16	1	US-08-307-724B-6	Sequence 6, App11
37	4	18.2	16	1	US-08-307-724B-7	Sequence 7, App11
38	4	18.2	16	1	US-08-307-724B-8	Sequence 8, App11
39	4	18.2	16	1	US-08-307-724B-9	Sequence 9, App11
40	4	18.2	16	1	US-08-307-724B-10	Sequence 10, App1
41	4	18.2	16	1	US-08-307-724B-11	Sequence 11, App1
42	4	18.2	16	1	US-08-307-724B-12	Sequence 12, App1
43	4	18.2	16	1	US-08-307-724B-13	Sequence 13, App1
44	4	18.2	16	1	US-08-307-724B-14	Sequence 14, App1
45	4	18.2	16	3	US-08-982-129-20	Sequence 20, App1

#### ALIGNMENTS

RESULT 1  
US-08-845-926-14  
Sequence 14, Application US/08845926  
Patent No. 5935778  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike  
APPLICANT: SCHMITT, Urban  
APPLICANT: JUNG, G. nther-Gerhard  
APPLICANT: IHLENFELDT, HANS-Georg  
TITLE OF INVENTION: Method for serological typing using  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845,926  
FILING DATE: 04-28-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/598,993  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 04 302.2  
FILING DATE: 09-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:





TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 22  
US-09-112-206-98

Query Match 54.58; Score 12; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASKQADIOPA 12  
Db 10 QASKQADIOPA 21

RESULT 5  
US-08-845-926-15  
Sequence 15, Application US/08845926  
Patent No. 5935778  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike  
APPLICANT: SCHMITT, Urban  
APPLICANT: JUNG, G other-Gerhard  
APPLICANT: IHLENFELDT, HANS-Georg  
APPLICANT: KRAAS, Wolfgang  
TITLE OF INVENTION: Method for serological typing using  
TITLE OF INVENTION: type-specific antigens  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Ofam LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845,926  
CLASSIFICATION: 435  
FILING DATE: 04-28-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/598,993  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 04 302.2  
FILING DATE: 09-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

ORIGINAL SOURCE:  
ORGANISM: Hepatitis C Virus  
US-08-845-926-15

Query Match 36.4%; Score 8; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QADIOPA 12  
Db 5 QADIOPA 12

RESULT 6  
US-08-146-028-97  
Sequence 97, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:  
APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPTIOPES AND THE  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYATE  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPTIOPES  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,028  
INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 22  
US-08-146-028-97

Query Match 27.3%; Score 6; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASKQA 6  
Db 16 QASKQA 21

RESULT 7  
US-08-146-028-153  
Sequence 153, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPTIOPES AND THE  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYATE  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPTIOPES  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,028  
INFORMATION FOR SEQ ID NO: 153:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Xaa is absent  
LOCATION: 1  
FEATURE:  
NAME/KEY: Xaa is absent  
LOCATION: 22  
US-08-146-028-153

Query Match 27.3%; Score 6; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASKQA 6  
Db 16 QASKQA 21

## RESULT 8

US-08-723-425A-97  
Sequence 97, Application US/08723425A  
Patent No. 6165730  
GENERAL INFORMATION:  
APPLICANT: DELEYS, ROBERT  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
NUMBER OF SEQUENCES: 453  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,425A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 22  
US-08-723-425A-97

Query Match 27.3%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASKQA 6  
Db 16 QASKQA 21

## RESULT 9

US-08-723-425A-153  
Sequence 153, Application US/08723425A  
Patent No. 6165730  
GENERAL INFORMATION:  
APPLICANT: DELEYS, ROBERT  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
NUMBER OF SEQUENCES: 453  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,425A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 153:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Xaa is absent  
LOCATION: 1  
FEATURE:  
NAME/KEY: Xaa is absent  
LOCATION: 22  
US-08-723-425A-153

Query Match 27.3%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QASKOA 6  
Db 16 QASKOA 21

## RESULT 10

US-09-112-206-97  
Sequence 97, Application US/09112206  
Patent No. 6210903

## GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112.206  
FILING DATE:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/146.028  
FILING DATE:

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide

HYPOTHEICAL: NO  
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:

NAME/KEY: Modified-site  
LOCATION: 1

FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 22

US-09-112-206-97

Query Match 27.3%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QASKOA 6  
Db 16 QASKOA 21

US-09-112-206-153  
Sequence 153, Application US/09112206  
Patent No. 6210903

## GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112.206  
FILING DATE:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/146.028  
FILING DATE:

INFORMATION FOR SEQ ID NO: 153:

SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO

ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:

NAME/KEY: Xaa is absent  
LOCATION: 1

FEATURE:  
NAME/KEY: Xaa is absent  
LOCATION: 22

US-09-112-206-153

Query Match 27.3%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QASKOA 6  
Db 16 QASKOA 21

## RESULT 12

US-08-127-909-11  
Sequence 11, Application US/08127909  
Patent No. 5436228

## GENERAL INFORMATION:

APPLICANT: Postlethwaite, Arnold E.  
APPLICANT: Seyer, Jerome  
APPLICANT: Kang, Andrew  
TITLE OF INVENTION: CHEMOTACTIC WOUND HEALING PEPTIDES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City

STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/127.909  
FILING DATE:

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 90202

TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-127-909-11

Query Match 22.7%; Score 5; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PKVEQ 22  
|||||  
Db 10 PKVEQ 14

RESULT 13  
US-08-127-909-13  
Sequence 13, Application US/08127909  
Patent No. 5436228  
GENERAL INFORMATION:  
APPLICANT: Postlethwaite, Arnold E.  
APPLICANT: Seyer, Jerome  
TITLE OF INVENTION: CHEMOTACTIC WOUND HEALING PEPTIDES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/127,909  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 90202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-127-909-13

Query Match 22.7%; Score 5; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PKVEQ 22  
|||||  
Db 10 PKVEQ 14

RESULT 14  
US-08-457-353-11  
Sequence 11, Application US/08457353  
Patent No. 5824647  
GENERAL INFORMATION:  
APPLICANT: Postlethwaite, Arnold E.

APPLICANT: Seyer, Jerome  
APPLICANT: Kang, Andrew  
TITLE OF INVENTION: CHEMOTACTIC WOUND HEALING PEPTIDES  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,353  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 90202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-457-353-11

Query Match 22.7%; Score 5; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 PKVEQ 22  
|||||  
Db 10 PKVEQ 14

RESULT 15  
US-08-457-353-13  
Sequence 13, Application US/08457353  
Patent No. 5824647  
GENERAL INFORMATION:  
APPLICANT: Postlethwaite, Arnold E.  
APPLICANT: Seyer, Jerome  
TITLE OF INVENTION: CHEMOTACTIC WOUND HEALING PEPTIDES  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,353  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 90202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-457-353-13

Query Match 22.7%; Score 5; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 18 PKVEQ 22  
Db 10 PKVEQ 14

Search completed: July 23, 2001, 16:56:53  
Job time: 270 sec

**This Page Blank (uspto)**

Jul 24 09:12:29 2001

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:56:12 ; Search time 65.41 Seconds  
(without alignments)  
20.390 Million cell updates/sec

Title: US-09-351-296-14

Perfect score: 22  
Sequence: 1 QASRQADIDPAPVQASMPKVEQ 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 148088

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

A\_Geneseq\_0601:\*

1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT:\*

2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT:\*

3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT:\*

4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT:\*

5: /SIDSR/gcgdata/geneseq/geneseq/AA1984.DAT:\*

6: /SIDSR/gcgdata/geneseq/geneseq/AA1985.DAT:\*

7: /SIDSR/gcgdata/geneseq/geneseq/AA1986.DAT:\*

8: /SIDSR/gcgdata/geneseq/geneseq/AA1987.DAT:\*

9: /SIDSR/gcgdata/geneseq/geneseq/AA1988.DAT:\*

10: /SIDSR/gcgdata/geneseq/geneseq/AA1989.DAT:\*

11: /SIDSR/gcgdata/geneseq/geneseq/AA1990.DAT:\*

12: /SIDSR/gcgdata/geneseq/geneseq/AA1991.DAT:\*

13: /SIDSR/gcgdata/geneseq/geneseq/AA1992.DAT:\*

14: /SIDSR/gcgdata/geneseq/geneseq/AA1993.DAT:\*

15: /SIDSR/gcgdata/geneseq/geneseq/AA1994.DAT:\*

16: /SIDSR/gcgdata/geneseq/geneseq/AA1995.DAT:\*

17: /SIDSR/gcgdata/geneseq/geneseq/AA1996.DAT:\*

18: /SIDSR/gcgdata/geneseq/geneseq/AA1997.DAT:\*

19: /SIDSR/gcgdata/geneseq/geneseq/AA1998.DAT:\*

20: /SIDSR/gcgdata/geneseq/geneseq/AA1999.DAT:\*

21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT:\*

22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	17 AAR99904	Hepatitis C Virus
2	12	54.5	22	14 AAR41155	HCV (type 2) pepti
3	9	40.9	22	17 AAR95551	Hepatitis C Virus
4	8	36.4	22	17 AAR99905	Hepatitis C Virus
5	6	27.3	22	14 AAR41154	HCV (type 2) pepti
6	5	22.7	12	19 AAR6731	Synthetic peptide
7	5	22.7	14	21 AAB08246	Peptide derived fr
8	5	22.7	14	21 AAY92979	Transforming growt
9	5	22.7	14	21 AAY92980	Transforming growt
10	5	22.7	22	16 AAR79198	TGF-beta1 residues
11	5	22.7	22	16 AAR79200	TGF-beta1 residues

12 22.7 22 19 AAM67264  
13 5 22.7 22 19 AAM67266  
14 4 18.2 6 17 AAM21373  
15 4 18.2 6 17 AAM05816  
16 4 18.2 7 21 AAB23230  
17 4 18.2 8 16 AAM21493  
18 4 18.2 8 16 AAR83814  
19 4 18.2 8 16 AAM59591  
20 4 18.2 8 19 AAY40601  
21 4 18.2 8 20 AAY40612  
22 4 18.2 8 21 AAB29940  
23 4 18.2 8 21 AAB29951  
24 4 18.2 8 21 AAB38495  
25 4 18.2 9 15 AAY51587  
26 4 18.2 9 15 AAY38090  
27 4 18.2 9 16 AAR83815  
28 4 18.2 9 16 AAR83816  
29 4 18.2 9 18 AAM45662  
30 4 18.2 9 20 AAY45658  
31 4 18.2 9 20 AAY46696  
32 4 18.2 9 20 AAY17976  
33 4 18.2 10 19 AAY20487  
34 4 18.2 10 19 AAM52477  
35 4 18.2 10 20 AAY46822  
36 4 18.2 10 20 AAY09667  
37 4 18.2 10 20 AAY00831  
38 4 18.2 10 21 AAB22783  
39 4 18.2 10 21 AAY73069  
40 4 18.2 12 13 AAR25629  
41 4 18.2 12 16 AAR62960  
42 4 18.2 12 16 AAY71740  
43 4 18.2 12 20 AAY31585  
44 4 18.2 12 20 AAM94416  
45 4 18.2 12 20 AAM95420

## ALIGNMENTS

RESULT 1  
ID AAR99904 standard; peptide: 22 AA.  
AC AAR99904:  
XX 23-APR-1997 (first entry)  
XX  
XX  
XX Hepatitis C Virus antigen peptide 14.  
DE  
XX HCV; immunologically reactive; antigen; epitope; screen; typing;  
KW antibody; immobilised.  
XX  
XX Hepatitis C Virus.  
OS  
XX  
XX EP726463-A2.  
XX  
XX 14-AUG-1996.  
XX  
XX 09-FEB-1996; 96EP-0101925.  
XX  
XX 09-FEB-1995; 95DE-4004302.  
XX  
XX (BOEF) BOEHRINGER MANNHEIM GMBH.  
XX  
XX Schmitt U, Seidel C, Wienhues-Chelen U;  
XX  
XX WPI; 1996-364504/37.  
XX  
XX Antibody typing by sequential reaction with immobilised antigens -  
XX esp. using new hepatitis C virus peptide(s) as antigens  
XX  
XX Claim 9; Page 14; 22pp; German.  
XX

CC AA998991-920 comprise at least one immunologically active region of  
CC hepatitis C virus (HCV), selected from amino acid sequences 384-414,  
CC 1738-1759, 221-2236, 2402-2419 and 2345-2357. The peptides are  
CC used in a claimed method for typing antibodies in a 14p sample.  
CC Assays performed using the peptides as antigens, which correspond  
CC to regions of high immunogenicity and variability, can be performed  
CC routinely using simple equipment to provide accurate HCV typing.  
CC AA9989901-06 are derived from amino acids 1738-1759 of the NS4-region  
CC of HCV.

50 Sequence 22 AA;

Query Match	100.0%	Score 22;	DB 17;	Length 22;
Best Local Similarity	100.0%	Pred. No. 7e-16;		
Matches 22; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0.

```
QY 1 QASKQADIDQPAVQASWPKVEQ 22
    |||||
Db 1 qaskqgadlqpavqaswmpkveq 22
```

## RESULT 2

ID	AAK41155	standard; peptide; 22 AA.
----	----------	---------------------------

AC AAR41155;

DT 22-MAR-1994 (first entry)

DE HCV (type 2) peptide XIV-2.

KW Human immunodeficiency virus; HIV; hepatitis C virus; HCV;  
 KW non-A non-B hepatitis; NANBH; human T-cell lymphotropic virus; HTLV;  
 KW epitope; antibody; biotin; diagnosis; detection; vaccine.  
 XX  
 XX  
 XX Synthetic.  
 XS

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

ET

/note= "the N-terminal comprises (A)-(B)-(X)-Y; where

B= biotin;  
X= biotinylation cpd. incorporated during synthesis;  
Y= bond or linking gp(s), which

whereby is not a bond it is pref. 1-10 residues of (same or different) glycine, beta-alanine, 4-aminobutyric acid, 5-aminovaleeric acid or 6-aminohexanoic acid; parentheses around B and X indicate opt. presence at the specified positions but B or X must be present in at least one of the positions shown, B interacts with the peptide to give a cpd. with greater diagnostic sensitivity;

FT	Modified-site	22
----	---------------	----

/note= "the C-terminal comprises Y-(X)-Z"

PN W09318054-A.

PD 16-SEP-1993

PF 08-MAR-1993; 93WO-EP00517.

PR 06-MAR-1992; 92EP-0400598.

PA (INNO-) INNOGENETICS NV SA.

PI De LEYS R;

XX  
DR WPI; 1993-303397/38.

PI New biotinylated peptide(s) corresp. to immuno-dominant  
 PT epitope(s) - with increased antigenicity, useful in antibodies  
 PT detection and vaccines against hepatitis C, HIV and HTLV  
 XX  
 PS Claim 4; Page 90-98; 133pp; English.

CC Peptide compans. comprise atleast one and pref. a combination of  
CC two, three, four or more biotinylated peptides chosen from the  
CC sequences given in AAR41058-R4166. The peptides represent  
CC immunologically important regions of viral proteins and are  
CC prep'd. by solid phase peptide synthesis. The compans. are  
CC useful for the detection of antibodies to HCV, and/or HIV,  
CC and/or H1N1-V-I or II.

Sequence 22 AA;

Query Match	54.5%	Score 12:	DB 14:	Length 22:
Best Local Similarity	100.0%	Pred. No.	7.5e-06:	
Matches 12, Conservative	0:	Mismatches	0:	Indels 0: Gaps 0:

```
QY 1 QASKQAQDIQA 12
    | | | | | | | |
Db 10 qaskqadlqpa 21
```

### RESULT 3

ID AAR95551 standard; Peptide; 22 AA.

AC AAR95551,

DT 26-SEP-1996 (first entry)

DE Hepatitis C Virus II Non-Structural protein 4 epitope.

KW HCV; hepatitis C virus; epitope; antigen; detection; chimera.

OS Hepatitis C virus.

PN JP08073497-A.

PD 19-MAR-1996.

PF 31-AUG-1994; 94JP-0232073.

PR 31-AUG-1994; 94JP-0232073.

PA (TOFU ) TONEN CORP.

DR WPI; 1996-205533/21.

PT New hepatitis C virus chimeric antigenic peptide - for the detection  
PT of hepatitis C virus infection or its group

CC The present sequence is that of a group II hepatitis C virus (HCV)  
CC non-structural protein 4 (NS4) epitope, designated 2-Y. Chimeras  
CC prepared by connecting at least two different epitopes on the group  
CC HCV-related antigen, encoded by the genomic RNA of HCV or its cDNA,  
CC through a peptide linkage, are useful for the specific detection of  
CC HCV infection.

SQ Sequence 22 AA;

Query Match	40.9%	Score 9;	DB 17;	Length 22;
Best Local Similarity	100.0%	Pred. No. 0.0077;		
Matches 9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;



OY 1 QASKROADI 9  
 DB 13 qaskqadgi 21

## RESULT 4

ID AAR99905 standard; peptide: 22 AA.

AC AAR99905;

DT 23-APR-1997 (first entry)

DE Hepatitis C Virus antigen peptide 15.

KW HCV; immunologically reactive; antigen; epitope; screen; typing; antibody; immobilised.

OS Hepatitis C Virus.

PN EP726463-A2.

PD 14-AUG-1996.

PF 09-FEB-1996; 96EP-0101925.

PR 09-FEB-1995; 95DE-4004302.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

PI Schmitt U, Seidel C, Wienhues-thelen U;

DR WPI; 1996-364504/37.

PT Antibody typing by sequential reaction with immobilised antigens - esp. using new hepatitis C virus peptide(s) as antigens

PS Claim 9; Page 15; 22pp; German.

CC AAR9891-920 comprise at least one immunologically active region of hepatitis C virus (HCV), selected from amino acid sequences 384-414, 1738-1759, 2217-2236, 2402-2419 and 2345-2357. The peptides are used in a claimed method for typing antibodies in a 11q sample. CC Assays performed using the peptides as antigens, which corresp. to CC regions of high immunogenicity and variability, can be performed CC routinely using simple equipment to provide accurate HCV typing. CC AAR9901-06 are derived from amino acids 1738-1759 of the NS4-region of HCV.

SQ Sequence 22 AA;

OY 5 QADIDIPA 12  
 DB 5 qadidipa 12

Query Match 36.4%; Score 8; DB 17; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.077; Mismatches 0; Gaps 0;  
 Matches 8; Conservative 0; Indels 0;

## RESULT 5

ID AAR41154 standard; peptide: 22 AA.

AC AAR41154;

DT 22-MAR-1994 (first entry)

DE HCV (type 2) peptide XIII-2 or NS4-7 (2).

KW Human immunodeficiency virus; HIV; hepatitis C virus; HCV;

KW non-A non-B hepatitis; NANBH; human T-cell lymphotropic virus; HTLV;  
 XX epitope; antibody; biotin; diagnosis; detection; vaccine.  
 OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "the N-terminal comprises (A)-(B)-(X)-Y; where

FT B= biotin;

FT X= biotinylation cpd. incorporated during synthesis;

FT Y= bond or linking gp(s), which minimises steric hindrance,

FT where Y is not a bond it is pref. 1-10 residues of (same or different) glycine,

FT 5-aminovaleic acid or 6-aminohexanoic acid; parentheses around B and X indicate opt. presence

FT at the specified positions but B or X must be present in at least one of the positions shown,

FT B interacts with the peptide to give a cpd. with greater diagnostic sensitivity;

FT A (optional)= one or more amino acids, NH2 or gp. which modifies the N-terminus;

FT Z= one or more amino acids, OH, NH2, or a linkage involving either of these 2 gps. "

FT Modified-site 22 /note= "the C-terminal comprises Y-(X)-Z"

FT WO9318054-A.

PD 16-SEP-1993.

PF 08-MAR-1993; 93WO-EP00517.

PR 06-MAR-1992; 92EP-0400598.

PA (INNO-) INNOGENETICS NV SA.

PI De LEYS R;

DR WPI; 1993-303397/38.

PT New biotinylated peptide(s) corresp. to immuno-dominant epitope(s) - with increased antigenicity, useful in antibodies

PT detection and vaccines against hepatitis C, HIV and HTLV

PS Claim 4; Page 90-98; 133pp; English.

CC Peptide compns. comprise at least one and pref. a combination of two, three, four or more biotinylated peptides chosen from the CC sequences given in AAR41058-R41166. The peptides represent CC immunologically important regions of viral proteins and are CC prepd. by solid phase peptide synthesis. The compns. are CC useful for the detection of antibodies to HCV, and/or HIV, and/or HTLV-I or II.

SQ Sequence 22 AA;

OY 1 QASKROA 6  
 DB 16 qaskqa 21

Query Match 27.3%; Score 6; DB 14; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 7.8; Mismatches 0; Conservative 0; Indels 0; Gaps 0;

OY 1 QASKROA 6  
 DB 16 qaskqa 21

## RESULT 6

ID AAW86731 standard; peptide: 12 AA.

AC AAW86731;  
XX  
PD 02-FEB-1999 (first entry)  
XX  
DE Synthetic peptide derived from TGF-beta.  
XX  
KW Transforming growth factor; TGF-beta-1; agonist; synergist;  
KM immunogen; immune modulation; antiinflammatory; autoimmune;  
XX wound healing; tissue repair.  
XX  
OS Synthetic.  
XX  
PN EP877031-A1.  
XX  
PD 11-NOV-1998.  
XX  
PF 06-MAY-1997; 97EP-0201342.  
XX  
PR 06-MAY-1997; 97EP-0201342.  
XX  
PA (DIER-) INST DIERHOUDERIJ EN DIERGEZONDHEID ID-DLO.  
XX  
DR WPI; 1998-570500/49.  
XX  
PT New Transforming Growth Factor mimicking peptides - useful for  
PT tissue repair and immune modulation in humans and animals  
XX  
PS Claims 5,7,8; Page 17; 23pp; English.  
XX  
CC The patent discloses (A) 14 new synthetic peptides derived from  
CC Transforming Growth Factor-beta (TGF-beta) which mimic TFG-beta  
CC activity; and (B) a pharmaceutical composition comprising TGF-beta-1  
CC and at least one of 16 defined synthetic peptides derived from TFG-beta  
CC which mimics its activity. Five of the 14 new peptides are amongst the  
CC 16 peptides used in the TGF-beta-1 composition. The novel peptides are  
CC agonists of TGF-beta, and the peptides in the TGF-beta-1 composition  
CC act as synergists for the TGF-beta-1. (A) and (B) are useful for  
CC treating immune or inflammatory disorders, e.g. allograft rejection,  
CC septic shock, adult respiratory disease syndrome (ARDS), autoimmune  
CC disease, rheumatoid arthritis, systemic lupus erythematosus (SLE) or  
CC inflammatory bowel disease. They can also be used in wound healing  
CC and as immunogens to elicit antibodies.  
CC The present sequence represents one of the peptides which can be used as  
CC a synergist in the TGF-beta-1 composition.  
XX  
SQ Sequence 12 AA:  
  
Query Match 22.7%; Score 5; DB 19; Length 12;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 18 PKVFD 22  
    |||||  
DB 1 pkveq 5

RESULT 7  
ID AAB08246 standard; peptide: 14 AA.  
XX  
AC AAB08246;  
XX  
DT 04-DEC-2000 (first entry)  
XX  
DE Peptide derived from a 40 kDa cell wall protein of Candida albicans.  
XX  
KW Cell wall protein; yeast infection; pathogenesis inhibitor;  
KM pathogenic yeast.  
XX  
OS Candida albicans.  
XX  
PN WO200048620-A1.

XX  
PD 24-AUG-2000.  
XX  
PF 18-FEB-2000; 2000MO-US04228.  
XX  
PR 19-FEB-1999; 99US-0120764.  
XX  
PR 19-FEB-1999; 99US-0120765.  
XX  
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.  
XX  
PI Hazen KC, Singleton DR, Masouka J, Wu JG, Glee PM;  
XX  
DR WPI; 2000-565334/52.  
XX  
PT New isolated hydrophobic protein antigens derived from the cell walls  
PT of Candida albicans and their corresponding antibodies, useful for  
PT detecting and treating yeast infection  
XX  
PS Disclosure; Page 12; 62pp; English.  
XX  
CC AAB08241-50 represent peptides which are derived from a 40 kDa cell  
CC wall protein of Candida albicans. The peptides have been identified  
CC by mass spectroscopy analysis. The cell wall peptides and their  
CC corresponding antibodies are useful for treating yeast infections in a  
CC patient, as well as for preventing or detecting infection of any yeast  
CC type. These include opportunistic and nosocomial infections. The  
CC peptides are also useful in the development of peptidomimetics and/or  
CC small organic molecules with therapeutic, diagnostic and/or research  
CC use. The antibodies are effective inhibitors of hydrophobically mediated  
CC pathogenesis events. They are also useful in diagnostic tests  
CC (i.e. detect, diagnose and serotype yeast infection), and for detecting  
CC the presence of Candida and other pathogenic yeasts, in a biological  
CC sample. Furthermore, they may be used as research and development tools.  
XX  
SQ Sequence 14 AA:  
  
Query Match 22.7%; Score 5; DB 21; Length 14;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 QPAVQ 14  
    |||||  
DB 3 qvavq 7

RESULT 8  
ID AAY92979 standard; peptide: 14 AA.  
XX  
AC AAY92979;  
XX  
DT 08-NOV-2000 (first entry)  
XX  
DE Transforming growth factor inhibitory peptide p25.  
XX  
KW Hepatotropic; antagonist; transforming growth factor betarl; TGF-b1;  
KW competitive inhibitor; collagen synthesis stimulation inhibitor; liver;  
KW extracellular matrix degradation inhibitor; mimotope; cirrhosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200031135-A1.  
XX  
PD 02-JUN-2000.  
XX  
PF 23-NOV-1999; 99WO-ES00375.  
XX  
PR 24-NOV-1998; 98ES-0002465.  
XX  
PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
XX  
PI Ezquerro Saenz JI, Lasarte Sagastibelza JU, Prieto Valtuena J;

PI Borras Cuesta F;  
 XX WPI; 2000-411935/35.  
 XX  
 PT Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are  
 PT partial sequences of the factor or its receptors  
 PS Disclosure; Page 23; 86pp; Spanish.  
 XX  
 CC The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor  
 CC in vivo which have partial amino acid sequences identical, or similar,  
 CC with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133  
 CC represent examples of the peptides of the invention. The peptides act  
 CC by competitive inhibition of the binding of TGF-b1 to its receptors,  
 CC e.g. they are inhibitors of stimulation of collagen synthesis in liver  
 CC cells and inhibitors of synthesis of proteolytic enzymes able to degrade  
 CC the extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of  
 CC liver disease, specifically cirrhosis.  
 XX  
 SQ Sequence 14 AA;  
 XX  
 Query Match 22.7%; Score 5; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 18 PKVEQ 22  
 |||||  
 Db 8 pkveq 12  
 XX  
 RESULT 9  
 ID AAY92980 standard; peptide; 14 AA.  
 XX  
 AC AAY92980;  
 DT 08-NOV-2000 (first entry)  
 XX  
 DE Transforming growth factor inhibitory peptide P26.  
 XX  
 KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200031135-A1.  
 XX  
 PD 02-JUN-2000.  
 PD  
 PF 23-NOV-1999; 99MO-ES00375.  
 XX  
 PR 24-NOV-1998; 98ES-0002465.  
 PR  
 PA (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.  
 PI  
 PI Ezguerra Saenz JI, Lasarte Sagastibelza JI, Prieto Valtuena J;  
 PI Borras Cuesta F;  
 DR WPI; 2000-411935/35.  
 XX  
 PT Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are  
 PT partial sequences of the factor or its receptors  
 PS Disclosure; Page 23; 86pp; Spanish.  
 XX  
 CC The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor

CC in vivo which have partial amino acid sequences identical, or similar,  
 CC with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133  
 CC represent examples of the peptides of the invention. The peptides act  
 CC by competitive inhibition of the binding of TGF-b1 to its receptors,  
 CC e.g. they are inhibitors of stimulation of collagen synthesis in liver  
 CC cells and inhibitors of synthesis of proteolytic enzymes able to degrade  
 CC the extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of  
 CC liver disease, specifically cirrhosis.  
 XX  
 SQ Sequence 14 AA;  
 XX  
 Query Match 22.7%; Score 5; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 18 PKVEQ 22  
 |||||  
 Db 4 pkveq 8  
 XX  
 RESULT 10  
 ID AAR79198 standard; peptide; 22 AA.  
 XX  
 AC AAR79198;  
 DT 06-MAR-1996 (first entry)  
 XX  
 DE TGF-betal residues 366-387.  
 XX  
 KW Chemotactic; transforming growth factor-beta; TGF-beta; fibroblast;  
 KW inflammatory cell; neutrophil; monocyte; macrophage; proliferation;  
 KW collagen synthesis; wound healing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5436228-A.  
 PD 25-JUL-1995.  
 PD  
 PF 12-DEC-1990; 90US-0626631.  
 XX  
 PR 28-SEP-1993; 93US-0127909.  
 PR 12-DEC-1990; 90US-0626631.  
 XX  
 PA (KANG/) KANG A.  
 PA (POST/) POSTLETHWAITE A E.  
 PA (SEYE/) SEYER J.  
 PI  
 PI Kang A, Postlethwaite AE, Seyer J;  
 DR WPI; 1995-268831/35.  
 XX  
 PT Novel chemotactic peptide(s) based on transforming growth  
 PT factor-beta - used to induce chemotaxis and proliferation of  
 PT fibroblasts and inflammatory cells, partic. for wound healing  
 PS Claim 4; Column 7; 28pp; English.  
 XX  
 CC The sequences given in AAR79188-207 are chemotactic peptides derived  
 CC from four overlapping regions of transforming growth factor (TGF)-beta  
 CC isoforms 1-5. These peptide correspond to the regions 368-374, 364-378,  
 CC 366-387 and 358-382 from the carboxy terminal portion of the TGF-beta  
 CC isoforms. The numbering of the positions of the peptides is based on  
 CC TGF-beta1. These peptides possess chemotactic properties for  
 CC fibroblasts and inflammatory cells, including neutrophils and  
 CC monocytes/macrophages. They also stimulate fibroblast proliferation  
 CC and collagen synthesis. They are partic. used to promote wound  
 CC healing.  
 XX  
 SQ Sequence 22 AA;  
 XX

Query Match 22.7%: Score 5; DB 16; Length 22;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 PKVEQ 22  
|||||  
DB 10 pkveq 14

## RESULT 11

AAR79200  
ID AAR79200 standard; peptide: 22 AA.

XX AAR79200;

XX 06-MAR-1996 (first entry)

XX TGF-beta3 residues 366-387.

XX Chemotactic; transforming growth factor-beta; TGF-beta; fibroblast;

KW inflammatory cell; neutrophil; monocyte; macrophage; proliferation;

KM collagen synthesis; wound healing.

XX Homo sapiens.

XX US5436228-A.

XX 25-JUL-1995.

XX 12-DEC-1990; 90US-0626631.

XX 28-SEP-1993; 93US-0127909.

PR 12-DEC-1990; 90US-0626631.

XX (KANG/) KANG A.

PA (POST/) POSTLETHWAITE A E.

PA (SEYE/) SEYER J.

XX Kang A, Postlethwaite AE, Seyer J;

PI WPI; 1995-268831/35.

DR Novel chemotactic peptide(s) based on transforming growth

XX factor-beta - used to induce chemotaxis and proliferation of

PT fibroblasts and inflammatory cells, partic. for wound healing

XX Claim 4; Column 7; 28pp; English.

PS The sequences given in AAR79188-207 are chemotactic peptides derived

XX from four overlapping regions of transforming growth factor (TGF)-beta

CC isoforms 1-5. These peptides correspond to the regions 368-374, 364-378,

CC 366-387 and 358-382 from the carboxy terminal portion of the TGF-beta

CC isoforms. The numbering of the positions of the peptides is based on

CC TGF-beta1. These peptides possess chemotactant properties for

CC fibroblasts and inflammatory cells, including neutrophils and

CC monocytes/macrophages. They also stimulate fibroblast proliferation

CC and collagen synthesis. They are partic. used to promote wound

CC healing.

CC Sequence 22 AA;

SQ

QY

DB

## RESULT 12

AAM67264  
ID AAM67264 standard; peptide: 22 AA.

XX AAM67264;

XX 21-DEC-1998 (first entry)

DE Peptide #11 with chemotactic activity.

XX Chemotactic activity; wound healing; transforming growth factor;

KW chemotaxis; fibroblast; collagen synthesis.

XX Synthetic.

OS Homo sapiens.

XX US5824647-A.

XX 20-OCT-1998.

XX 12-DEC-1990; 90US-0626631.

XX 01-JUN-1995; 95US-0457353.

PR 12-DEC-1990; 90US-0626631.

PR 28-SEP-1993; 93US-0127909.

XX (KANG/) KANG A.

PA (POST/) POSTLETHWAITE A E.

PA (SEYE/) SEYER J.

XX Kang A, Postlethwaite AE, Seyer J;

PI WPI; 1998-582597/49.

DR Chemotactic peptide(s) for e.g. wound healing - corresponding to

XX fragments of transforming growth factor beta isoforms

PT Disclosure; Column 3; 34pp; English.

XX The invention relates to chemotactic peptides which are used for inducing

CC chemotaxis of fibroblasts and/or inflammatory cells in vitro or in vivo;

CC for inducing proliferation of fibroblasts and/or inflammatory cells in

CC vitro or in vivo; for inducing collagen synthesis by fibroblasts in vitro

CC or in vivo; and for promoting wound healing. The present sequence

CC represents a chemotactic peptide disclosed in the specification.

XX Sequence 22 AA;

SQ

QY

DB

QY 18 PKVEQ 22

|||||

DB 10 pkveq 14

RESULT 13

AAM67266

ID AAM67266 standard; peptide: 22 AA.

XX AAM67266;

XX 21-DEC-1998 (first entry)

DE Peptide #13 with chemotactic activity.

XX Chemotactic activity; wound healing; transforming growth factor;

KW chemotaxis; fibroblast; collagen synthesis.

XX Synthetic.

OS Homo sapiens.

XX US5824647-A.  
 PN 20-OCT-1998.  
 XX  
 PD  
 XX  
 PE 12-DEC-1990; 90US-0626631.  
 XX  
 PR 01-JUN-1995; 95US-0457353.  
 PR 12-DEC-1990; 90US-0626631.  
 PR 28-SEP-1993; 93US-0127909.  
 XX  
 PA (KANG/) KANG A.  
 PA (POST/) POSTLETHWAITE A E.  
 PA (SEYE/) SEYER J.  
 XX  
 PI Kang A, Postlethwaite AE, Seyer J;  
 XX  
 DR WPI: 1998-582597/49.  
 PT  
 PT Chemotactic peptide(s) for e.g. wound healing - corresponding to  
 PT fragments of transforming growth factor beta isoforms  
 XX  
 PS Disclosure; Column 3; 34pp; English.  
 CC  
 CC The invention relates to chemotactic peptides which are used for inducing  
 CC chemotaxis of fibroblasts and/or inflammatory cells in vitro or in vivo;  
 CC for inducing proliferation of fibroblasts and/or inflammatory cells in  
 CC vitro or in vivo; for inducing collagen synthesis by fibroblasts in vitro  
 CC or in vivo; and for promoting wound healing. The present sequence  
 CC represents a chemotactic peptide disclosed in the specification.  
 XX  
 SQ Sequence 22 AA;

Query Match 22.7%; Score 5; DB 19; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 79;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 18 PKVEQ 22  
 |||||  
 Db 10 pkveq 14

RESULT 14  
 AAW21373  
 ID AAW21373 standard; peptide: 6 AA.  
 XX  
 AC AAW21373;  
 XX  
 DT 29-JUL-1997 (first entry)  
 XX  
 DE Plasmalogen activator inhibitor 1 derived signal oligopeptide #1.  
 XX  
 KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;  
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;  
 KW charge; polarity; farnesyl synthetase; plasmalogen activator inhibitor 1;  
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;  
 KW gonadoliberin precursor; plasmalogen activator inhibitor 2; prorenin;  
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;  
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;  
 KW treponema pallidum membrane protein; TPA; islet amyloid polypeptide;  
 KW fibroblast MMP1; schistosoma elastase precursor; schistosomn;  
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9519568-A1.  
 XX  
 PD 20-JUL-1995.  
 XX  
 PE 12-JAN-1995; 95WO-US00575.  
 XX

PR 14-JAN-1994; 94US-0182248.  
 XX  
 PA (RATH/) RATH M.  
 XX  
 PI Rath M;  
 XX  
 DR WPI: 1995-263953/34.  
 XX  
 PR Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
 PR regions of max. hydrophilicity, used in modulating communication  
 PR between proteins(s)  
 PT  
 PS Claim 5; Page 51; 88pp; English.  
 XX  
 CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-  
 CC peptides. These signal oligopeptides are localised on the surface  
 CC of the protein and are represented by the hydrophilicity maxima of  
 CC the protein. These peptides are enriched in charged amino acids  
 CC arranged with neutral spacer amino acids. The specific signal  
 CC character of these oligopeptides is determined by a characteristic  
 CC combination of conformation and charge within the signal sequence.  
 CC These oligopeptides may be used as vaccines in the treatment of  
 CC human disease, as competitive inhibitors to prevent or reduce the  
 CC metabolic action or interaction of a selected protein by blocking  
 CC its specific signal sequences, or as therapeutic agents to function  
 CC as feedback regulators to reduce synthesis rate of a selected protein.  
 CC These peptides may be modified by omitting one or more amino acids at  
 CC the N- and/or C-terminal, by substituting one or more amino acids  
 CC without consideration of charge and polarity, by substituting one or  
 CC more amino acids with amino acid residues with similar charge and/or  
 CC polarity, by omitting one or more amino acids or a combination of these.  
 XX  
 SQ Sequence 6 AA;

Query Match 18.2%; Score 4; DB 16; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QASK 4  
 |||||  
 Db 1 qask 4

RESULT 15  
 AAW05816  
 ID AAW05816 standard; peptide: 6 AA.  
 XX  
 AC AAW05816;  
 XX  
 DT 09-JUL-1997 (first entry)  
 XX  
 DE TNFalpha residues 29-34 antitense peptide aFNTIII.  
 XX  
 KW Antitense peptide; hydrophatic peptide; antagonist; interleukin-1beta;  
 KW IL-1beta; cytokine; cancer; inflammatory condition; rheumatoid arthritis;  
 KW septic shock; therapy; IL-1alpha; IL-8; tumour necrosis factor alpha;  
 KW TNFalpha; ectatin.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9634887-A2.  
 XX  
 PD 07-NOV-1996.  
 XX  
 PE 07-MAY-1996; 96WO-GB01082.  
 XX  
 PR 11-APR-1996; 96GB-0007505.  
 PR 05-MAY-1995; 95GB-0009263.  
 XX  
 PA (UNLO ) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.  
 PA (UNLO ) LONDON SCHOOL HYGIENE & TROPICAL MEDICIN.  
 XX

PI Miller AD, Raynes JG;  
XX  
DR WPI: 1996-506102/50.

XX Anti:sense peptide(s) which alter the activities of target  
PT cytokine(s) - used to treat inflammatory conditions e.g. rheumatoid  
PT arthritis or cancer  
XX

PS Claim 10; Page 29; 41pp; English.

XX  
CC AA05812-W05819 represent antisense peptides of the invention. Antisense  
CC peptides are encoded by antisense DNA. The antisense peptides are the  
CC hydrophobic complement of the peptides encoded by the sense DNA strand.  
CC Antisense peptides exert an antagonistic effect on target ligands by  
CC virtue of their ability to bind to the sense peptide sequences, and  
CC thereby competing with the normal binding ligands for the peptide. These  
CC sequences are antisense to a target polypeptide, and when bound to their  
CC targets, alter the biological activity of the target polypeptide or the  
CC activity of a target molecule containing the peptide. AA05814-W05816  
CC are antisense to a sequence contained within tumour necrosis factor  
CC alpha (TNFalpha). These sequences are used to treat or prevent  
CC conditions mediated by cytokines, preferably cancer or inflammatory  
CC conditions, especially rheumatoid arthritis or septic shock.  
XX

SQ Sequence 6 AA;

Query Match 18.2%; Score 4; DB 17; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PAVQ 14  
|||  
Db 3 pavq 6

Search completed: July 23, 2001, 16:56:12  
Job time: 529 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 17:06:05 ; Search time 69.82 Seconds

(without alignments)  
41.689 Million cell updates/sec

Title: US-09-351-296-13

Perfect score: 22

Sequence: 1 TATKQAEAAAPVESKMRALV 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 425026 segs, 132305027 residues

Word size: 0

Total number of hits satisfying chosen parameters: 5654

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

SPTREMBL.16:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp rodent:\*  
12: sp.unclassified:\*  
13: sp.vertebrate:\*  
14: sp.virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	18.2	7	2	047477 escherichia
2	4	18.2	11	2	09K332 staphylococ
3	4	18.2	11	4	014759 homo sapien
4	4	18.2	11	4	09UCR1 pseudorabie
5	4	18.2	13	14	069394 bos taurus
6	4	18.2	15	6	09TC09 bos taurus
7	4	18.2	15	6	09TR40 bos taurus
8	4	18.2	15	8	09TR50 nicotiana t
9	4	18.2	15	11	09OUZ5 mus sp. 38-
10	4	18.2	16	2	09KHM6 synechococc
11	4	18.2	16	10	09S8L1 sorghum bic
12	4	18.2	16	10	P82161 spinacia ol
13	4	18.2	16	11	09QZV3 mus musculu
14	4	18.2	16	11	09QUY8 cricetus
15	4	18.2	17	11	061932 mus musculu
16	4	18.2	19	6	097584 macaca mula
17	4	18.2	19	10	P81895 solanum tub
18	4	18.2	19	14	069396 pseudorabie
19	4	18.2	20	2	069176 chlamydia t

20	4	18.2	20	2	053520 chlamydia t
21	4	18.2	20	2	085509 chlamydia t
22	4	18.2	20	2	085510 chlamydia t
23	4	18.2	20	2	085512 chlamydia t
24	4	18.2	20	2	085514 chlamydia t
25	4	18.2	20	2	085517 chlamydia t
26	4	18.2	20	2	085519 chlamydia t
27	4	18.2	20	2	085520 chlamydia t
28	4	18.2	20	2	085521 chlamydia t
29	4	18.2	20	2	085522 chlamydia t
30	4	18.2	20	2	085523 chlamydia t
31	4	18.2	20	2	085525 chlamydia t
32	4	18.2	20	2	085526 chlamydia t
33	4	18.2	20	2	085528 chlamydia t
34	4	18.2	20	2	085530 chlamydia t
35	4	18.2	20	2	085531 chlamydia t
36	4	18.2	20	2	085533 chlamydia t
37	4	18.2	20	2	09R525 thermus aqu
38	4	18.2	20	4	09UOH2
39	4	18.2	20	9	037944 lactococcus
40	4	18.2	20	11	09QV80 ratius sp.
41	4	18.2	21	8	09ZYX6 orussus ter
42	4	18.2	22	2	P81150 desulfovibr
43	4	18.2	22	2	09RAQ3 pseudomonas
44	4	18.2	22	5	09TWJ8 crithidia f
45	4	18.2	22	13	09PS65 oncorhynch

## ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	7 AA.
047477	047477			
AC	047477			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE	TPI PROTEIN (FRAGMENT).			
GN	TPI.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
NCBI	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE OF 7-7 FROM N.A.			
RX	MEDLINE=65203917; PubMed=3158524;			
RA	Hellings H.W., Evans P.R.;			
RT	"Nucleotide sequence and high-level expression of the major			
RT	Escherichia coli phosphofructokinase.";			
RL	Eur. J. Biochem. 149:363-373(1985).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RA	Evans P.;			
RL	Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.			
DR	EMBL, X02519; CAA26359.1; -.			
FT	NON_TER			
FT	1			
SO	SEQUENCE			
SO	7 AA; 773 MW; 7416D33DDDBIDB0 CRC64;			
Query Match	18.2%;	Score 4;	DB 2;	Length 7;
Best Local Similarity	100.0%;	Pred. No. 4.2e+05;		
Matches	4;	Conservative	0;	Mismatches
Matches	0;	Indels	0;	Gaps
Matches	0;			
QY	6 AEAA 9			
QY				
Db	1 AEAA 4			
RESULT	2			
ID	09K332	PRELIMINARY:	PRT:	11 AA.
AC	09K332:			

DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE GEN (FRAGMENT).  
 CN GEN.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 CC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VARIOUS STRAINS;  
 RX MEDLINE=20187516; PubMed=10722640;  
 RA Cremon S.E., Schnell N.F., Goltz F., Bruckner R.;  
 RT "Identification of a new repetitive element in Staphylococcus  
 RT aureus.";  
 RL Infect. Immun. 68:2344-2348(2000).  
 DR EMBL; AF195967; AAF60251.1; -;  
 DR EMBL; AF195963; AAF60243.1; -;  
 DR EMBL; AF195964; AAF60245.1; -;  
 DR EMBL; AF195965; AAF60247.1; -;  
 DR EMBL; AF195966; AAF60249.1; -;  
 DR InterPro: IPR001189; -;  
 DR ProDom: PD000475; -; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 11 AA; 1262 MW; 4F978F86AAB1A723 CRC64;

Query Match 18.2%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TKQA 6  
 Db 8 TKQA 11

RESULT 3  
 ID 014759 PRELIMINARY; PRT; 11 AA.  
 AC 014759;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)  
 DE LYMPHOCYTE CYTOSOLIC PROTEIN 2 (FRAGMENT).  
 GN LCP2.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sunden S.L.F., Carr L.L., Clements J.L., Molto D.G., Koretzky G.A.;  
 RL Genomics 0:0-0(0).  
 DR EMBL; U44065; AAA93308.1; -;  
 FT NON\_TER 1  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1242 MW; D695104224072DD CRC64;

Query Match 18.2%; Score 4; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAA 9  
 Db 2 AEAA 5

RESULT 4  
 ID 09UCR1 PRELIMINARY; PRT; 11 AA.  
 AC 09UCR1;

DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
 DE AUTOTAXIN.  
 CN AUTOTAXIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=92129337; PubMed=1733949;  
 RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cloce V.,  
 RA Schiffrman E., Liotta L.A.;  
 RT "Identification, purification, and partial sequence analysis of  
 RT autotaxin, a novel motility-stimulating protein.";  
 RL J. Biol. Chem. 267:2524-2529(1992).  
 SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match 18.2%; Score 4; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATK 4  
 Db 8 TATK 11

RESULT 5  
 ID 069394 PRELIMINARY; PRT; 13 AA.  
 AC 069394;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
 DE GLYCOPROTEIN PRECURSOR (FRAGMENT).  
 OS Pseudorabies virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 CC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxID=10345;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93227568; PubMed=8385840;  
 RA Ryan P., Robbins A., Whealy M., Enquist L.W.;  
 RT "Overall signal sequence hydrophobicity determines the in vivo  
 RT translocation efficiency of a herpesvirus glycoprotein.";  
 RL Virus Genes 7:5-21(1993).  
 DR EMBL; M77773; AAA73134.1; -;  
 KW SIGNAL.  
 FT SIGNAL 1 12 POTENTIAL.  
 FT CHAIN 13 >13 POTENTIAL.  
 FT NON\_TER 13  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1274 MW; 7D36E7528A6F9DC4 CRC64;

Query Match 18.2%; Score 4; DB 14; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAP 11  
 Db 10 AAP 13

RESULT 6  
 ID 09TOQ9 PRELIMINARY; PRT; 15 AA.  
 AC 09TOQ9;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE GLUTAMATE DEHYDROGENASE ISOFORM I (EC 1.4.1.2) (FRAGMENT).  
 OS Bos taurus (Bovine).



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96061967; PubMed=7588764;  
 RA Cho S.W., Lee J., Choi S.Y.;  
 RT "Two soluble forms of glutamate dehydrogenase isoproteins from bovine  
 brain.";  
 RL Eur. J. Biochem. 233:340-346(1995).  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE=96043916; PubMed=7581004;  
 RA Lee J., Kim S.W., Cho S.W.;  
 RT "A novel glutamate dehydrogenase from bovine brain: purification and  
 characterization.";  
 RL Biochem. Mol. Biol. Int. 36:1087-1096(1995).  
 SQ SEQUENCE 15 AA; 1754 MW; 65F7CD91023AEBA CRC64;

Query Match 18.2%; Score 4; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAAA 10  
 Db 2 EAAA 5

RESULT 7  
 O9TR40  
 ID O9TR40 PRELIMINARY; PRT; 15 AA.  
 AC O9TR40;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE GLUTAMATE DEHYDROGENASE ISOFORM II (EC 1.4.1.2) (FRAGMENT).  
 OS Bos taurus (Bovinae).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96061967; PubMed=7588764;  
 RA Cho S.W., Lee J., Choi S.Y.;  
 RT "Two soluble forms of glutamate dehydrogenase isoproteins from bovine  
 brain.";  
 RL Eur. J. Biochem. 233:340-346(1995).  
 SQ SEQUENCE 15 AA; 1724 MW; 65F7CD91023AE925 CRC64;

Query Match 18.2%; Score 4; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAAA 10  
 Db 2 EAAA 5

RESULT 8  
 O9T210  
 ID O9T210 PRELIMINARY; PRT; 15 AA.  
 AC O9T210;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE 18.5 KDA PHOTOSYSTEM I PSAD PROTEIN (FRAGMENT).  
 OS Nicotiana tomentosiformis (Tobacco).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
 OC Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4098;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94105345; PubMed=8278548;  
 RA Obokata J., Mikami K., Hayashida N., Nakamura M., Sugiyama M.;  
 RT "Molecular heterogeneity of photosystem I. psad, psaf, psah, and  
 psal are all present in isoforms in Nicotiana spp.";  
 RL Plant Physiol. 102:1259-1267(1993).  
 SQ SEQUENCE 15 AA; 1429 MW; D238E48B5760A8 CRC64;

Query Match 18.2%; Score 4; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAAA 10  
 Db 3 EAAA 6

RESULT 9  
 O9QUZ5  
 ID O9QUZ5 PRELIMINARY; PRT; 15 AA.  
 AC O9QUZ5;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE 38-42 KDA COSTIMULATORY FACTOR (FRAGMENT).  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96007483; PubMed=7559503;  
 RA Vinay D.S., Raju M., Verma R.K., Mishra G.C.;  
 RT "Characterization of novel costimulatory molecules. A protein of 38-42  
 kDa from B cell surface is concerned with T cell activation and  
 differentiation.";  
 RL J. Biol. Chem. 270:23429-23436(1995).  
 SQ SEQUENCE 15 AA; 1758 MW; F10C664C976A5D19 CRC64;

Query Match 18.2%; Score 4; DB 11; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEA 9  
 Db 2 AEA 5

RESULT 10  
 O9KHM6  
 ID O9KHM6 PRELIMINARY; PRT; 16 AA.  
 AC O9KHM6;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE PROTEOLYSIS TAG (FRAGMENT).  
 OS Synechococcus sp. PCC 6307.  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
 OX NCBI\_TaxID=59930;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20345063; PubMed=10884408;  
 RA Keller K.C., Shapiro L., Williams K.P.;  
 RT "tmRNAs that encode proteolysis-inducing tags are found in all known  
 bacterial genomes: A two-piece tmRNA functions in Caulobacter.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:7778-7783(2000).  
 DR EMBL; AF251551; AAF87980.1; -.

FT NON\_TER 1 1  
SQ SEQUENCE 16 AA: 1685 MW: 76245B0FB9AC6C62 CRC64;

Query Match 18.2%; Score 4; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 AAPV 12  
|||  
Db 11 AAPV 14

RESULT 11  
O9S8L1  
ID O9S8L1 PRELIMINARY; PRT; 16 AA.

AC O9S8L1 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
DE CYTOCHROME P-450 (FRAGMENT).  
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
Mangoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;  
OC Andropogoneae; Sorghum.  
NX NCBI\_TaxID=4558;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95024036; PubMed=7937883;  
RA Sribesen O., Koch B., Halkier B.A., Moller B.L.;  
RT "Isolation of the heme-thiolate enzyme cytochrome P-450<sub>TYR</sub>, which  
catalyzes the committed step in the biosynthesis of the cyanogenic  
glucoside dhurrin in Sorghum bicolor (L.) Moench.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:9740-9744(1994).  
SQ SEQUENCE 16 AA: 1516 MW: D5488D8AE99FD489 CRC64;

Query Match 18.2%; Score 4; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 ENAA 10  
|||  
Db 6 ENAA 9

RESULT 12  
P82161  
ID P82161 PRELIMINARY; PRT; 16 AA.

AC P82161 01-JUN-2000 (TREMBlrel. 14, Created)  
DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S10 BETA (FRAGMENT).  
OS Spinacia oleracea (Spinach).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
Mangoliophyta; eudicotyledons; core eudicots; Caryophyllidae;  
OC Caryophyllales; Chenopodiaceae; Spinacia.  
NX NCBI\_TaxID=3562;  
RN [1]  
RP SEQUENCE.  
RX STRAIN=CV. ALMARO; TISSUE=LEAF;  
MEDLINE=20435797; PubMed=10874039;  
RA Yamaguchi K., von Kroblaub K., Subramanian A.R.;  
RT "The plastid ribosomal proteins. Identification of all the proteins in  
the small subunit of an organelle ribosome (chloroplast).";  
RL J. Biol. Chem. 37:28455-28465(2000).  
CC -1 SUBCELLULAR LOCATION: CHLOROPLAST.  
CC -1 TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
CC -1 MISCELLANEOUS: THERE ARE TWO FORMS DUE MAYBE TO A DIFFERENT  
TRANSIT PEPTIDE CLEAVAGE.  
CC -1 MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 18.2 KDA.  
CC -1 SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.

DR InterPro: IPR001848;  
DR PROSITE: PS00361; RIBOSOMAL\_S10; PARTIAL.  
KW Ribosomal protein; Chloroplast.  
FT NON\_TER 16  
SQ SEQUENCE 16 AA: 1666 MW: 4B7BE4270EF59B27 CRC64;

Query Match 18.2%; Score 4; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 ALEV 22  
|||  
Db 2 ALEV 5

RESULT 13  
O9Q2Y3  
ID O9Q2Y3 PRELIMINARY; PRT; 16 AA.

AC O9Q2Y3 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE R29144/1 (FRAGMENT).  
GN R29144/1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=129;  
MEDLINE=99330555; PubMed=10400995;  
RA Smith D.P., Spicer J., Smith A., Swift S., Ashworth A.;  
RT "The mouse pcutz-jeghens syndrome gene lkb1 encodes a nuclear protein  
kinase.";  
RL Hum. Mol. Genet. 8:1479-1485(1999).  
DR EMBL: AF145697; AAD55370.1;  
FT NON\_TER 1  
SQ SEQUENCE 16 AA: 1518 MW: D6C720E4BFF0A1D2 CRC64;

Query Match 18.2%; Score 4; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 AAP 11  
|||  
Db 5 AAP 8

RESULT 14  
O9Q0Y8  
ID O9Q0Y8 PRELIMINARY; PRT; 16 AA.

AC O9Q0Y8 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE HISTONE H1 (FRAGMENT).  
OS Cricetus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetus.  
NX NCBI\_TaxID=10029;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96070893; PubMed=7499230;  
RA Guiley L.R., Valdez J.G., Buchanan J.S.;  
RT "Characterization of the mitotic specific phosphorylation site of  
histone H1. Absence of a consensus sequence for the p34cdc2/cyclin B  
kinase.";  
RL J. Biol. Chem. 270:27653-27660(1995).  
SQ SEQUENCE 16 AA: 1479 MW: 75EB488737288C8A CRC64;

Query Match 18.2%; Score 4; DB 11; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAP 11  
 1111  
 Db 9 AAP 12

## RESULT 15

Q61932  
 ID 061932 PRELIMINARY; PRT; 17 AA.  
 AC 061932;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT FAST (ADULT SKELETAL MUSCLE  
 DE MYOSIN HEAVY CHAIN) (FRAGMENT).  
 GN MYH4 OR MYH5F.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RX MEDLINE=84061805; Pubmed=6196357;  
 RA Weydert A., Dambas P., Caravatti M., Minty A., Bugalsky G., Cohen A.,  
 RA Robert B., Buckingham M.E.;  
 RT "Sequential accumulation of mRNAs encoding different myosin heavy  
 RT chain isoforms during skeletal muscle development in vivo detected  
 RT with a recombinant plasmid identified as coding for an adult fast  
 RT myosin heavy chain from mouse skeletal muscle.";  
 RL J. Biol. Chem. 258:13867-13874(1983).  
 DR EMBL; K00986; AAA39792.1; -;  
 DR MGD; MGI:1339713; Myh4.  
 KM Myosin.  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1985 MW; 40EA696BF87181E2 CRC64;

Query Match 18.2%; Score 4; DB 11; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 VES 15  
 1111  
 Db 6 VES 9

Search completed: July 23, 2001, 17:06:06  
 Job time: 547 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 17:04:49 ; Search time 23.18 Seconds

(Without alignments)  
32.512 Million cell updates/sec

Title: US-09-351-296-13

Perfect score: 22

Sequence: 1 TATKQEAAPVYESKMRLEY 22

Scoring table: OLIGO

Searched: 93435 seqs, 34255486 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1176

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	27.3	13	PSAE_PEA	P20118 pisum sativ
2	5	22.7	14	UBAL_CANFA	P99503 canis fami
3	4	18.2	13	BLAC_STRGR	P81173 streptomyc
4	4	18.2	14	YMTF_XANCP	003397 xanthomonas
5	4	18.2	15	UC06_MAIZE	P80613 zea mays (m
6	4	18.2	15	UN04_PINPS	P81673 pinus pinas
7	4	18.2	17	A45K_MYCBO	P80069 mycobacteri
8	4	18.2	21	LE04_BIOGL	P80743 biophalar
9	4	18.2	22	SETB_SALTY	P33027 salmonella
10	3	13.6	8	CLP_THICU	P80488 thiodacillu
11	3	13.6	9	DCML_PSRFC	P19913 pseudomonas
12	3	13.6	10	O20G_CONTE	P80466 comamonas t
13	3	13.6	13	CH60_CANFA	P49818 canis fami
14	3	13.6	13	CXET_CONTE	P81755 conus texti
15	3	13.6	13	FIBA_CAVPO	P14445 cavia porce
16	3	13.6	13	LIGA_TRAVE	P20011 tirametes ve
17	3	13.6	13	LIGH_TRAVE	P20012 tirametes ve
18	3	13.6	13	PSAU_PEA	P17229 pisum sativ
19	3	13.6	13	PSBP_PINPS	P81668 pinus pinas
20	3	13.6	14	PH1_PROSE	P29263 prunus sero
21	3	13.6	14	UC15_MAIZE	P80621 zea mays (m
22	3	13.6	14	UN07_CLOPA	P81332 clostridium
23	3	13.6	15	ATP2_SPIOU	P80083 spiniacia ol
24	3	13.6	15	ESTB_SCHGA	P81011 schizaphis
25	3	13.6	15	PH3_PROSE	P29265 prunus sero
26	3	13.6	15	SODM_ENTAE	P22799 enterobacte
27	3	13.6	15	UC08_MAIZE	P80613 zea mays (m
28	3	13.6	15	URE2_MORMO	P7338 morganella
29	3	13.6	16	FENR_STRGR	P4114 streptomyc
30	3	13.6	16	HTPG_ACTCA	P81876 acinetobact
31	3	13.6	16	PH2_PROSE	P29264 prunus sero
32	3	13.6	16	PSAU_SPIOU	P17230 spiniacia ol
33	3	13.6	17	ATP1_PAVLU	P28529 pavlova lut

34	3	13.6	17	1	GAST_MACMU	P33714 macaca mula
35	3	13.6	17	1	LPW_BRELA	P06556 brevbacter
36	3	13.6	17	1	SRY_URSAR	P36396 ursus arcto
37	3	13.6	17	1	VESP_VESMC	P57672 vespa mac
38	3	13.6	18	1	NPA_BOVIN	P15506 bos taurus
39	3	13.6	18	1	OBP_LYMDI	P34173 lymantria d
40	3	13.6	19	1	ATPB_CANFA	P99504 canis fami
41	3	13.6	19	1	H3_NARPS	P80553 narcissus p
42	3	13.6	19	1	HBB2_UROHA	P18992 uronastylx h
43	3	13.6	19	1	HHP_THICU	P80487 thiodacillu
44	3	13.6	19	1	PHLC_STAIN	P80924 staphylococ
45	3	13.6	19	1	PSAE_CUCSA	P42047 cucumis sat

## ALIGNMENTS

RESULT	ID	PSAE_PEA	STANDARD	PRT	13 AA.
AC	P20118	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	01-JUL-1993 (Rel. 26, Last annotation update)				
DE	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV (PHOTOSYSTEM I 13 KDA PROTEIN) (PSI-E) (FRAGMENT).				
CN	PSAE.				
OS	Pisum sativum (Garden pea).				
OC	Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids I:				
OC	Fabales: Fabaceae: Papilionoideae: Pisum.				
OX	NCBI_TaxID=3888;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=88137587; Pubmed=3277857;				
RA	Dunn P.P.J., Packman L.C., Pappin D., Gray J.C.;				
RT	"N-terminal amino acid sequence analysis of the subunits of pea photosystem I."				
RL	FEBS Lett. 228:157-161(1988).				
CC	-I- FUNCTION: MAY FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-				
CC	-I- OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.				
CC	-I- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE.				
CC	-I- SIMILARITY: BELONGS TO THE PSAE FAMILY.				
DR	PIR: S00316; S00316.				
KW	Photosynthesis; Photosystem I; Chloroplast; Thylakoid membrane.				
FT	NON_TER.				
SO	SEQUENCE 13 AA: 1190 MW; D895A63A52DBDID CRC64;				
Query Match 27.3%; Score 6; DB 1; Length 13;					
Best Local Similarity 100.0%; Pred. No. 3.5;					
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	6 AEAAP 11				
Db	6 AEAAP 11				
RESULT 2					
ID	UBAL_CANFA	STANDARD;	PRT;	14 AA.	
AC	P99503;				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	15-JUL-1998 (Rel. 36, Last annotation update)				
DE	UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT 11) (FRAGMENT).				
OS	Canis familiaris (Dog).				
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:				
OC	Mammalia: Eutheria: Carnivora: Fissipedia: Canidae; Canis.				
OX	NCBI_TaxID=9615;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Heart;				

```

RX MEDLINE-98163340; Pubmed-9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.3, ITS MW IS: 19.6 KDA.
DR HSC-2DPAGE; P95503; DOG.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1149 MW; 3D923888D8668C7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 5; DB 1; Length 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAAA 10
DB 1 AEAAA 5

RESULT 3
BLAC_STRGR STANDARD; PRT; 13 AA.
AC P81173;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE BETA-LACTAMASE (EC 3.5.2.6) (FRAGMENT).
OS Streptomyces griseus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1911;
RN [1]
RP SEQUENCE.
RC STRAIN-NRRL B-2682;
RX MEDLINE-98386507; Pubmed-9720038;
RA Deak E., Szabo I., Kalmanczheyl A., Gal Z., Barabas G.,
RA Panyige A.;
RT "Membrane-bound and extracellular beta-lactamase production with
RT developmental regulation in Streptomyces griseus NRRL B-2682.";
RL Microbiology 144:2169-2177(1998).
CC -1- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)O = A SUBSTITUTED BETA-
CC AMINO ACID.
CC -1- SUBCELLULAR LOCATION: SECRETED AND MEMBRANE-BOUND.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
DR Interpro: IPR000871;
DR PROSITE: PS00146; BETA_LACTAMASE_A; PARTIAL.
KW Hydrolase; Antibiotic resistance; Membrane.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1236 MW; 14C5129118D54760 CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 1; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAP 11
DB 1 AAAP 4

RESULT 4
YMPF_XANCP STANDARD; PRT; 14 AA.
AC Q03397;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE HYPOTHETICAL PROTEIN IN FRUK 5'REGION (ORF1) (FRAGMENT).
GN MTP.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;

```

```

OC Xanthomonas.
OX NCBI_TaxId=340;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92011547; Pubmed-1655739;
RA de Crecy-Lagard V., Bouvet O.M., Lejeune P., Danchin A.;
RT "Fructose catabolism in Xanthomonas campestris pv. campestris.
RT Sequence of the prs operon, characterization of the fructose-specific
RT enzymes.";
RU J. Biol. Chem. 266:18154-18161(1991).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M69242; AAA27600.1; -.
DR PIR: C40944; C40944.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1585 MW; 72EA9AA3CE16CCDB CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 1; Length 14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 RALE 21
DB 4 RALE 7

RESULT 5
UC06_MAIZE STANDARD; PRT; 15 AA.
ID UC06_MAIZE
AC P80612;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLOGICAL COLEOPTILE (SPOT 1131)
DE (FRAGMENT).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
OC Andropogoneae; Zea.
OX NCBI_TaxId=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morlin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.8, ITS MW IS: 71.0 KDA.
DR MaizeDB: P80612; COLEOPTILE.
DR MaizeDB: 123930; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 15 AA; 1390 MW; 7005E22830F23D61 CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 1; Length 15;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAP 11
DB 2 AAAP 5

```

RESULT 6  
UN04\_PINPS STANDARD; PRT; 15 AA.  
AC P81673;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N143) (FRAGMENT).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Coniferales; Coniferales; Pinaceae; Pinus.  
OX NCBI\_Taxid=71647;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Needle;  
RX MEDLINE=99274088; PubMed=10344291;  
RA Costa P., Plomieu C., Bauw G., Dubos C., Bahran N., Kremer A.,  
RA Figerio J.-M., Plomieu C.;  
RT "Separation and characterization of needle and xylem maritime pine  
RT proteins.";  
RL Electrophoresis 20:1098-1108(1999).  
CC -1- INDUCTION: BY WATER-STRESS.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.2, ITS MW IS: 21 KDA.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA: 1489 MW; CEAD85E9308227A CRC64;

Query Match 18.2%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EAAA 10  
Db 6 EAAA 9

RESULT 7  
A45K\_MYCBO STANDARD; PRT; 17 AA.  
ID A45K\_MYCBO  
AC P80069;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE 45/47 KDA ANTIGEN (FRAGMENT).  
OS Mycobacterium bovis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_Taxid=1765;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=BCG / PARIS 1173 P2;  
RX MEDLINE=93138802; PubMed=8423100;  
RA Romani F., Laqueyrie A., Miltzer P., Pescher P., Chavarot P.,  
RA Lagranderie M., Auregan G., Gheorghiu M., Marchal G.A.;  
RT "Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen  
RT complex, an immunodominant target for antibody response after  
RT immunization with living bacteria.";  
RL Infect. Immun. 61:742-750(1993).  
CC -1- SUBCELLULAR LOCATION: SECRETED.  
CC -1- SIMILARITY: TO M.LEPRAE N143, AND M.TUBERCULOSIS MPT32.  
DR PIR: A49237; A49237.  
KW Antigen.  
FT NON\_TER 17 17  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA: 1521 MW; 4492CC389D9893 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAAP 11  
Db 12 AAAP 15

RESULT 8  
LE04\_BIOGL STANDARD; PRT; 21 AA.  
ID LE04\_BIOGL  
AC P80743;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE HEMOLYMPH 65 KDA LECTIN BC04 (FRAGMENT).  
OS BG04.  
GN Blomphalaria glabrata (Bloodfluke planorb).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
OC Planorbidae; Blomphalaria.  
OX NCBI\_Taxid=6526;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=M-LINE; TISSUE=Hemolymph;  
RX MEDLINE=97385165; PubMed=9238039;  
RA Adema C.M., Hertel L.A., Miller R.D., Loker E.S.;  
RT "A family of fibrinogen-related proteins that precipitates parasite-  
RT derived molecules is produced by an invertebrate after infection.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:8691-8696(1997).  
CC -1- FUNCTION: BINDS AND PRECIPITATES ANTIGENS OF THE PARASITE  
CC ECHINOSTOMA PARANSEI.  
CC -1- SUBCELLULAR LOCATION: SECRETED IN THE HEMOLYMPH.  
KW Lectin.  
FT NON\_TER 1 1  
FT NON\_TER 21 21  
SQ SEQUENCE 21 AA: 2239 MW; B8593D7A4902858C CRC64;

Query Match 18.2%; Score 4; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 VVES 15  
Db 13 VVES 16

RESULT 9  
SETB\_SALTY STANDARD; PRT; 22 AA.  
ID SETB\_SALTY  
AC P33027;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE SUGAR EFFLUX TRANSPORTER B (FRAGMENT).  
GN SETB.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Salmonella.  
OX NCBI\_Taxid=602;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89313694; PubMed=2546043;  
RA Geerse R.H., Izso F., Postma P.W.;  
RT "The PEP: fructose phosphotransferase system in Salmonella  
RT typhimurium: Fpt combines enzyme IIFru and pseudo-Hfr activities.";  
RL Mol. Gen. Genet. 216:517-525(1989).  
CC -1- FUNCTION: INVOLVED IN THE EFFLUX OF SUGARS. THE PHYSIOLOGICAL ROLE  
CC MAY BE THE DETOXIFICATION OF NON-METABOLIZABLE SUGAR ANALOGS. CAN  
CC TRANSPORT LACTOSE AND GLUCOSE (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE  
CC (PROBABLE).  
CC -1- SIMILARITY: BELONGS TO THE SET FAMILY OF TRANSPORTERS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; X14243; -; NOT\_ANNOTATED\_CDS.

KM StyEgE; SG10423; setB. Transmembrane; Inner membrane.

FT TRANSMEM 13 >22 POTENTIAL.

FT NON\_TER 22  
SQ SEQUENCE 22 AA: 2291 MW: 2849C330172C5C2 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AAP 11  
Db 7 AAP 10

RESULT 10

CLP\_THICU STANDARD: PRT: 8 AA.

AC P80488:

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE CHEMOLITHOTROPH-SPECIFIC PROTEIN (FRAGMENT).

OS Thiobacillus cuprinus.

CC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Thiomonas.

NCBI\_TaxID=36860;

RN [1]

RP SEQUENCE.

RC STRAIN=DSM 5494;

RA Martin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;

RL Submitted (SEP-1995) to the SWISS-PROT data bank.

CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED

CC CHEMOLITHOTROPHICALLY.

FT NON\_TER 8  
SQ SEQUENCE 8 AA: 785 MW: 91487B06DCC2D76D CRC64;

Query Match 13.6%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 APV 12  
Db 1 APV 3

RESULT 11

DCML\_PSECF STANDARD: PRT: 9 AA.

AC P19913:

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-DEC-1992 (Rel. 24, Last annotation update)

DE CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).

OS Pseudomonas carboxydoflava.

CC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;

CC Hydrogenophaga.

NCBI\_TaxID=47421;

OX [1]

RN SEQUENCE.

RP MEDLINE=90055678; PubMed=2818128;

RA Kraut M., Hugendieck I., Herwig S., Meyer O.;

RT "Homology and distribution of CO dehydrogenase structural genes in

RT carboxydotrophic bacteria.";

RL Arch. Microbiol. 152:335-341(1989).

CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED

CC ACCEPTOR.

CC -1- COFACTOR: MOLYBDENUM.

CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND

CC SMALL.

DR PIR; P10139; P10139.

KW Oxidoreductase; Molybdenum.

FT VARIANT 2 2 N -> M.

FT NON\_TER 9 9

SQ SEQUENCE 9 AA: 974 MW: 0224DAB6C2D76DD4 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 APV 12  
Db 3 APV 5

RESULT 12

Q20G\_COMTE STANDARD: PRT: 10 AA.

AC P80466:

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE QUINOLINE 2-OXIDOREDUCTASE, GAMMA CHAIN (EC 1.-.-.-) (FRAGMENT).

OS Comamonas testosteroni (Pseudomonas testosteroni).

CC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.

NCBI\_TaxID=285;

RN [1]

RP SEQUENCE.

RC STRAIN=63;

RA MEDLINE=96035889; PubMed=7556204;

RT Schach S., Tshisuaka B., Fetzner S., Lingsen F.;

RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-

RT dioxxygenase from Comamonas testosteroni 63. The first two enzymes in

RT quinoline and 3-methylquinoline degradation.";

RL Eur. J. Biochem. 232:536-544(1995).

CC -1- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-

CC 1,2-DIHYDROQUINOLINE.

CC -1- COFACTOR: FAD AND MOLYBDENUM.

CC -1- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND

CC (3-METHYL-)-QUINOLINE.

CC -1- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND

CC TWO GAMMA CHAINS (PROBABLE).

KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.

FT NON\_TER 10 10

SQ SEQUENCE 10 AA: 1153 MW: C848CE64433B1DC6 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 QAE 7  
Db 3 QAE 5

RESULT 13

CH60\_CANFA STANDARD: PRT: 13 AA.

AC P49818:

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP60) (60 KDA CHAPERONIN)

(CPN60) (HEAT SHOCK PROTEIN 60) (HSP-60) (MITOCHONDRIAL MATRIX PROTEIN



DE P1) (FRAGMENT).  
 GN HSPD1 OR HSP60.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND  
 MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF  
 IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE  
 REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED  
 UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.  
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
 DR HSC-2DPAGE: P49818; DOG.  
 DR InterPro: IPR001844;...  
 DR PROSITE: PS00296; CHAPERONINS\_CPN60; PARTIAL.  
 KM Chaperone; ATP-binding; Mitochondrion.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1383 MW; C6571E012DBFE879 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 RAL 20  
 DB 11 RAL 13

RESULT 14  
 CXXET\_CONTE  
 ID CXXET\_CONTE STANDARD: PRT; 13 AA.  
 AC P81755;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE EPSILON-CONOTOXIN TXIX;  
 OS Conus textile (Clutch-of-gold cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 CC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=6494;  
 RN [1]  
 RP SEQUENCE, CARBOHYDRATE-LINKAGE SITE THR-10, AND STRUCTURE BY NMR.  
 RC TISSUE=Venom.  
 RX MEDLINE=99254114; PubMed=10318957;  
 RA Ribby A.C., Lucas-Meunier E., Kalume D.E., Czerwicz E., Hambe B.,  
 Dahlqvist I., Fossier P., Baux G., Roepstorff P., Baleja J.D.,  
 RA Furie B.C., Furie B., Stenflo J.P.;  
 RT "A conotoxin from Conus textile with unusual posttranslational  
 modifications reduces presynaptic Ca2+ influx.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5758-5763(1999).  
 CC -1- FUNCTION: CONOTOXIN WHICH ACTS AT PRESYNAPTIC MEMBRANES, BLOCKING  
 THE CALCIUM CHANNELS.  
 CC -1- PM: O-GLYCAN CONSISTS OF THE DISACCHARIDE GAL-GALNAC.  
 DR PDB: 1WCT; 08-JUN-99.  
 KM Presynaptic neurotoxin; Calcium channel inhibitor; Venom; Vitamin K;  
 KM Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Bromination;  
 KW 3D-structure.  
 FT DISULFID 2 8  
 FT DISULFID 3 9  
 FT MOD\_RES 1 1 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 4 4 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 7 7 BROMINATION.  
 FT MOD\_RES 13 13 HYDROXYLATION.

FT CARBOHYD 10 10 O-LINKED (GALNAC...);  
 SQ SEQUENCE 13 AA; 1388 MW; 386C9E1C74AFA378 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAP 11  
 DB 11 AAP 13

RESULT 15  
 FTBA\_CAVPO  
 ID FTBA\_CAVPO STANDARD: PRT; 13 AA.  
 AC P14445;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-JAN-1990 (Rel. 13, Last annotation update)  
 DE FIBRINOPEPTIDE A.  
 DE Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Hystriognathli; Cavidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE.  
 RA Blomback B., Blomback M., Grondahl N.J.;  
 RT "Studies on fibrinopeptides from mammals.";  
 RL Acta Chem. Scand. 19:1789-1791(1965).  
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 AGGREGATION  
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 KM Blood coagulation; Plasma.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1309 MW; 639999286C79DDDB CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAA 9  
 DB 6 EAA 8

Search completed: July 23, 2001, 17:04:49  
 Job time: 510 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:57:40 ; Search time 41.27 Seconds

(without alignments)  
40.607 Million cell updates/sec

Title: US-09-351-296-13

Perfect score: 22

Sequence: 1 TATKQAEAAAPVYESKRALEV 22

Scoring table: OLIGO

Searched: 219241 seqs, 76174552 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4035

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database: PIR\_68:\*

1: pir1:\*\n2: pir2:\*\n3: pir3:\*\n4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27.3	13	2	S00316	photosystem I 13K
2	22.7	12	2	PN0577	tyrosine 3-monooxy
3	22.7	12	2	PN0578	tyrosine 3-monooxy
4	22.7	12	2	PN0579	tyrosine 3-monooxy
5	22.7	12	2	PN0580	tyrosine 3-monooxy
6	22.7	12	2	PN0581	tyrosine 3-monooxy
7	22.7	12	2	PN0576	tyrosine 3-monooxy
8	22.7	15	2	PN0577	light harvesting c
9	22.7	22	2	PC7072	H+-transporting AT
10	18.2	10	2	PE50209	24k protein 4407 -
11	18.2	11	2	H54346	pyruvate synthase
12	18.2	12	2	PN0696	1,4-alpha-glucan b
13	18.2	13	2	A38929	glutathione peroxi
14	18.2	14	2	C40944	hypothetical prote
15	18.2	15	2	PA00692	photosystem I 18.5
16	18.2	15	2	PA00694	adenylate isopente
17	18.2	15	2	PT00094	succinate dehydrog
18	18.2	16	2	S36876	equaebalamin redu
19	18.2	17	2	T55226	myosin heavy chain
20	18.2	17	2	A4896	heat shock protein
21	18.2	17	2	A49237	45/47K antigen - M
22	18.2	18	2	PT0239	ig heavy chain CDR
23	18.2	19	2	I53673	amyloid protein -
24	18.2	20	2	PN0154	groEL-like protein
25	18.2	20	2	A42267	J-kappa recombinat
26	18.2	22	2	PQ0667	photosystem I 19.3
27	18.2	22	2	D47256	kinetoplast DNA-as
28	13.6	6	2	B60110	repetitive protein
29	13.6	6	2	JH0784	neuropeptide TE-6

30	3	13.6	8	2	T48890	hypothetical prote
31	3	13.6	8	2	S68325	blood cell protein
32	3	13.6	9	2	S66608	quinoline 2-oxidor
33	3	13.6	9	2	PL0139	carbon-monoxide de
34	3	13.6	9	2	A43848	cell surface adhes
35	3	13.6	9	2	S66635	alpha-2-macroglobu
36	3	13.6	9	2	B38740	ig kappa chain C r
37	3	13.6	9	4	S15594	orf 1 rara 5'-regi
38	3	13.6	10	2	S69159	cystathionine gamm
39	3	13.6	10	2	PQ0783	MDH dehydrogenase
40	3	13.6	10	2	B61440	polygalacturonase
41	3	13.6	10	2	S19617	globin - polychaet
42	3	13.6	10	2	I52645	gene B-50 protein
43	3	13.6	10	2	C54226	light-harvesting p
44	3	13.6	11	2	PQ0682	photosystem I 17.5
45	3	13.6	11	2	PC4267	ribosomal protein

#### ALIGNMENTS

RESULT 1  
S00316  
Photosystem I 13K protein - garden pea (fragment)  
C:Species: Pisum sativum (garden pea)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 18-Jun-1993  
C:Accession: S00316; PT0019  
R:Dunn, P.P.J.; Packman, L.C.; Pappin, D.; Gray, J.C.  
FEBS Lett. 228, 157-161, 1988  
A:Title: N-terminal amino acid sequence analysis of the subunits of pea photosystem I  
A:Reference number: S00314; MUID:86137587  
A:Accession: S00316  
A:Molecule type: protein  
A:Residues: 1-13 <DUN>  
C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match Best Local Similarity 27.3%; Score 6; DB 2: Length 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEAAAP 11  
DB 6 AEAAAP 11

RESULT 2  
PN0577  
tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - gorilla (fragment)

N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase  
C:Species: Gorilla gorilla (gorilla)  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000  
R:Chinoone, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.  
Biochem. Biophys. Res. Commun. 195, 158-165, 1993

A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.  
A:Reference number: PN0575; MUID:93371398  
A:Accession: PN0577  
A:Molecule type: genomic RNA  
A:Residues: 1-12 <ICB>

A:Cross-references: GB:I14795  
A:Experimental source: lymphocytes of peripheral blood  
C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine bi  
C:Superfamily: phenylalanine 4-monooxygenase  
C:Keywords: bipterin; monooxygenase; oxidoreductase

Query Match Best Local Similarity 22.7%; Score 5; DB 2: Length 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4 KOAEA 8  
|||||

Db 6 KOAEA 10

RESULT 3

PM0578

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - orangutan (fragment)  
N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase  
C:Species: Pongo pygmaeus (orangutan)  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000  
C:Accession: PM0578  
R:Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.  
Biochem. Biophys. Res. Commun. 195, 158-165, 1993  
A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.  
A:Reference number: PM0575; MUID:93371398  
A:Accession: PM0578  
A:Molecule type: genomic RNA  
A:Residues: 1-12 <ICP>  
A:Cross-references: GB:L14798  
A:Experimental source: lymphocytes of peripheral blood  
C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis.  
C:Superfamily: phenylalanine 4-monooxygenase  
C:Keywords: bipterin; monooxygenase; oxidoreductase

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 55;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KOAEA 8

|||||

Db 6 KOAEA 10

RESULT 4

PM0579

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - common gibbon (fragment)  
N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase  
C:Species: Hylobates lar (common gibbon, white-handed gibbon)  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000  
C:Accession: PM0579  
R:Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.  
Biochem. Biophys. Res. Commun. 195, 158-165, 1993  
A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.  
A:Reference number: PM0575; MUID:93371398  
A:Accession: PM0579  
A:Molecule type: genomic RNA  
A:Residues: 1-12 <ICP>  
A:Cross-references: GB:L14792  
A:Experimental source: lymph nodes  
C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis.  
C:Superfamily: phenylalanine 4-monooxygenase  
C:Keywords: bipterin; monooxygenase; oxidoreductase

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 55;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KOAEA 8

|||||

Db 6 KOAEA 10

RESULT 5

PM0580

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - Japanese macaque (fragment)  
N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase  
C:Species: Macaca fuscata (Japanese macaque)  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000  
C:Accession: PM0580  
R:Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.  
Biochem. Biophys. Res. Commun. 195, 158-165, 1993  
A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.

A:Reference number: PM0575; MUID:93371398

A:Accession: PM0580

A:Molecule type: genomic RNA

A:Residues: 1-12 <ICP>

A:Cross-references: GB:L14804

A:Experimental source: kidney

C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis.

C:Superfamily: phenylalanine 4-monooxygenase

C:Keywords: bipterin; monooxygenase; oxidoreductase

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 55;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KOAEA 8

|||||

Db 6 KOAEA 10

RESULT 6

PM0581

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - common marmoset (fragment)  
N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase  
C:Species: Callithrix jacchus (common marmoset)  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000  
C:Accession: PM0581  
R:Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.  
Biochem. Biophys. Res. Commun. 195, 158-165, 1993  
A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.  
A:Reference number: PM0575; MUID:93371398  
A:Accession: PM0581  
A:Molecule type: genomic RNA  
A:Residues: 1-12 <ICP>  
A:Cross-references: GB:L14803  
A:Experimental source: kidney  
C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis.  
C:Superfamily: phenylalanine 4-monooxygenase  
C:Keywords: bipterin; monooxygenase; oxidoreductase

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 55;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KOAEA 8

|||||

Db 6 KOAEA 10

RESULT 7

PM0576

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - chimpanzee (fragment)  
N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000  
C:Accession: PM0576  
R:Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.  
Biochem. Biophys. Res. Commun. 195, 158-165, 1993  
A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.  
A:Reference number: PM0575; MUID:93371398  
A:Accession: PM0576  
A:Molecule type: genomic RNA  
A:Residues: 1-12 <ICP>  
A:Cross-references: GB:L14789  
A:Experimental source: lymphocytes of peripheral blood  
C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis.  
C:Superfamily: phenylalanine 4-monooxygenase  
C:Keywords: bipterin; monooxygenase; oxidoreductase

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 55;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 KOEA 8  
 |||||  
 Db 6 KOEA 10

RESULT 8  
 PT0037  
 light harvesting complex chain III/b, photosystem I - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993  
 C:Accession: PT0037; PS0205  
 R:Uchiyama, Y.; Tsugita, A.  
 submitted to JIPID, June 1991  
 A:Reference number: PS0189  
 A:Accession: PT0037  
 A:Molecule type: protein  
 A:Residues: 1-15 <UCH>

Query Match 22.7%; Score 5; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EAAAP 11  
 |||||  
 Db 4 EAAAP 8

RESULT 9  
 PC7072  
 H+-transporting ATP synthase (EC 3.6.1.34) delta chain, mitochondrial - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
 C:Accession: PC7072  
 R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;  
 Electrophoresis 21, 1853-1871, 2000  
 A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t  
 A:Reference number: PC7072  
 A:Accession: PC7072  
 A:Molecule type: protein  
 A:Residues: 1-22 <TSD>  
 A:Experimental source: strain C57BL/6Cr SLC, male; brain, striatum  
 C:Keywords: brain; hydrolase; mitochondrion

Query Match 22.7%; Score 5; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAAA 10  
 |||||  
 Db 1 AEAAA 5

RESULT 10  
 PS0209  
 24K protein 4407 - rice (strain Nihonbare) (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
 C:Accession: PS0209  
 R:Tsugita, A.; Kamo, M.  
 submitted to JIPID, April 1993  
 A:Reference number: PS0209  
 A:Accession: PS0209  
 A:Molecule type: protein  
 A:Residues: 1-10 <TSD>  
 A:Experimental source: callus  
 C:Comment: molecular weight 24K; pI 4.6.

Query Match 18.2%; Score 4; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 4; 6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEAA 9  
 |||||  
 Db 7 AEAA 10

RESULT 11  
 H54346  
 pyruvate synthase (EC 1.2.7.1) alpha chain - Pyrococcus furiosus (fragment)  
 C:Species: Pyrococcus furiosus  
 C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-May-2000  
 C:Accession: H54346  
 R:Blamey, J.M.; Adams, M.W.  
 Biochemistry 33, 1000-1007, 1994  
 A:Title: Characterization of an ancestral type of pyruvate ferredoxin oxidoreductase  
 A:Reference number: A54346; MUID:94137707  
 A:Accession: H54346  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-11 <BLA>  
 C:Keywords: coenzyme A; oxidoreductase

Query Match 18.2%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EAAA 10  
 |||||  
 Db 7 EAAA 10

RESULT 12  
 PQ0696  
 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) [imported] - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C:Accession: PQ0696  
 R:Komatsu, S.; Kajiwara, H.; Hirano, H.  
 Theor. Appl. Genet. 86, 935-942, 1993  
 A:Title: A rice protein library; a data-file of rice proteins separated by two-dimens  
 A:Reference number: PQ0696  
 A:Accession: PQ0696  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <KOM>  
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 18.2%; Score 4; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5; 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EAAA 10  
 |||||  
 Db 1 EAAA 4

RESULT 13  
 A38929  
 glutathione peroxidase (EC 1.11.1.9) - sheep (fragment)  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 31-Oct-1997  
 C:Accession: A38929  
 R:Gettins, P.; Dyal, D.; Crews, B.  
 Arch. Biochem. Biophys. 294, 511-518, 1992  
 A:Title: Selenium-dependent glutathione peroxidases from ovine and bovine erythrocyte  
 A:Reference number: S21712; MUID:92231574  
 A:Accession: A38929  
 A>Status: preliminary  
 A:Molecule type: protein

A:Residues: 1-13 <GET>  
 C:Superfamily: glutathione peroxidase  
 C:Keywords: oxidoreductase

Query Match 18.2%; Score 4; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 8 AAP 11  
 ||||  
 Db 7 AAP 10

## RESULT 14

C40944  
 hypothetical protein (1-phosphofructokinase 5' region) - Xanthomonas campestris pv. camp  
 C:Species: Xanthomonas campestris pv. campestris  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 18-Jun-1999  
 C:Accession: C40944  
 R:de Crecy-Lagard, V.; Bouvet, O.M.M.; Lejeune, P.; Danchin, A.  
 J. Biol. Chem. 266, 18154-18161, 1991  
 A:Title: Fructose catabolism in Xanthomonas campestris pv. campestris. Sequence of the F  
 A:Reference number: A40944; MUID:92011547  
 A:Accession: C40944  
 A:Molecule type: DNA  
 A:Residues: 1-14 <DE3>  
 A:Cross-references: GB:M69242; NID:g155366; PIDN:AAA27600.1; PID:g155367  
 C:Superfamily: fructose phosphotransferase multiphosphoryltransfer protein; phosphotrans  
 sphotransferase system phosphonistidine-containing protein homology

Query Match 18.2%; Score 4; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 RALE 21  
 ||||  
 Db 4 RALE 7

## RESULT 15

P00692  
 photosystem I 18.5K D2 chain - tobacco (Nicotiana tomentosiformis) (fragment)  
 C:Species: Nicotiana tomentosiformis  
 C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
 C:Accession: P00692  
 R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiyura, M.  
 Plant Physiol. 102, 1259-1267, 1993  
 A:Title: Molecular heterogeneity of photosystem I. psad, psae, psaf, psah and psal are  
 A:Reference number: P00667; MUID:94105345  
 A:Accession: P00692  
 A:Molecule type: protein  
 A:Residues: 1-15 <OBO>  
 C:Superfamily: photosystem I chain II  
 C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 18.2%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAAA 10  
 ||||  
 Db 3 EAAA 6

Search completed: July 23, 2001, 16:57:40  
 Job time: 282 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:56:52 ; Search time 34.6 Seconds  
(without alignments)  
12.809 Million cell updates/sec

Title: US-09-351-296-13

Perfect score: 22  
Sequence: 1 TATKQAEAAAPVSEKRALEY 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 193259 .segs, 20144635 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93443

Minimum DB seq length: 6  
Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

1: Issued\_patents\_AA: \*  
2: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/PCBUS.COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	US-08-845-926-13	Sequence 13, App1
2	18	81.8	22	US-08-845-926-16	Sequence 16, App1
3	5	22.7	7	US-08-630-645-25	Sequence 25, App1
4	5	22.7	7	PCT-US96-10220-25	Sequence 25, App1
5	5	22.7	9	US-08-658-639-3	Sequence 3, App1
6	5	22.7	9	US-08-944-604-3	Sequence 3, App1
7	5	22.7	12	US-08-176-500-15	Sequence 15, App1
8	5	22.7	12	US-08-471-052A-15	Sequence 15, App1
9	5	22.7	12	US-08-381-960-9	Sequence 9, App1
10	5	22.7	12	US-08-189-331-15	Sequence 15, App1
11	5	22.7	12	US-08-471-839-15	Sequence 15, App1
12	5	22.7	12	US-08-471-800-15	Sequence 15, App1
13	5	22.7	12	US-08-471-068-15	Sequence 15, App1
14	5	22.7	12	US-08-630-645-24	Sequence 24, App1
15	5	22.7	12	PCT-US96-10220-24	Sequence 24, App1
16	5	22.7	13	US-08-632-514C-25	Sequence 25, App1
17	5	22.7	13	US-08-188-177-25	Sequence 25, App1
18	5	22.7	14	US-08-340-203A-14	Sequence 14, App1
19	5	22.7	14	US-08-452-427-14	Sequence 14, App1
20	5	22.7	14	US-09-085-407-14	Sequence 14, App1
21	5	22.7	16	US-08-660-592-3	Sequence 3, App1
22	5	22.7	16	US-08-660-592-8	Sequence 8, App1
23	5	22.7	16	US-09-166-930A-3	Sequence 3, App1
24	5	22.7	17	US-07-591-988B-1	Sequence 1, App1
25	5	22.7	17	US-07-591-988B-2	Sequence 1, App1
26	5	22.7	17	US-07-591-988B-3	Sequence 3, App1
27	5	22.7	17	US-07-591-988B-4	Sequence 4, App1

28	5	22.7	17	US-07-591-988B-5	Sequence 5, App1
29	5	22.7	17	US-08-164-618-2	Sequence 2, App1
30	5	22.7	17	US-08-164-618-3	Sequence 3, App1
31	5	22.7	17	US-08-164-618-4	Sequence 4, App1
32	5	22.7	17	US-08-006-037-1	Sequence 1, App1
33	5	22.7	17	US-08-006-037-2	Sequence 2, App1
34	5	22.7	17	US-08-006-037-3	Sequence 3, App1
35	5	22.7	17	US-08-006-037-4	Sequence 4, App1
36	5	22.7	17	US-08-006-037-5	Sequence 5, App1
37	5	22.7	17	US-08-955-206-4	Sequence 4, App1
38	5	22.7	17	US-08-614-377A-11	Sequence 11, App1
39	5	22.7	17	US-08-955-050-4	Sequence 4, App1
40	5	22.7	17	US-09-142-648B-11	Sequence 11, App1
41	5	22.7	19	US-08-660-592-4	Sequence 4, App1
42	5	22.7	19	US-08-660-592-5	Sequence 5, App1
43	5	22.7	19	US-09-166-930A-4	Sequence 4, App1
44	5	22.7	19	US-09-166-930A-5	Sequence 5, App1
45	5	22.7	20	US-08-602-999A-157	Sequence 157, App1

#### ALIGNMENTS

RESULT 1  
US-08-845-926-13  
Sequence 13, Application US/08845926  
Patent No. 5935778  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike  
APPLICANT: SCHMITT, Urban  
APPLICANT: JUNG, G nther-Gerhard  
APPLICANT: IHLENFELDT, HANS-Georg  
APPLICANT: KRAAS, Wolfgang  
TITLE OF INVENTION: Method for serological typing using  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/845,926  
FILING DATE: 04-28-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/598,993  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 04 302.2  
FILING DATE: 09-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SRO ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:

ORGANISM: Hepatitis C Virus  
US-08-845-926-13

Query Match 100.0%; Score 22; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TATKQEAAPVVEKMRLEV 22  
Db 1 TATKQEAAPVVEKMRLEV 22

RESULT 2  
US-08-845-926-16  
Sequence 16, Application US/08845926  
Patent No. 5935778

GENERAL INFORMATION:  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike  
APPLICANT: SCHMITT, Urban  
APPLICANT: JUNG, G. nther-gerhard  
APPLICANT: IHLENFELDT, HANS-Georg  
APPLICANT: KRAAS, Wolfgang  
TITLE OF INVENTION: Method for serological typing using  
TITLE OF INVENTION: type-specific antigens  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845, 926  
FILING DATE: 04-28-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/598, 993.  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 04 302.2  
FILING DATE: 09-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Hepatitis C Virus  
US-08-845-926-16

Query Match 81.8%; Score 18; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TATKQEAAPVVEKMR 18  
|||||

Db 1 TATKQEAAPVVEKMR 18

RESULT 3

US-08-630-645-25  
Sequence 25, Application US/08630645  
Patent No. 5948763  
GENERAL INFORMATION:  
APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
APPLICANT: FRANGIONE, Bias  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630, 645  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478, 326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA-1  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-630-645-25

Query Match 22.7%; Score 5; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPV 13  
Db 1 AAPV 5  
|||||

RESULT 4  
PCT-US96-10220-25  
Sequence 25, Application PC/TUS9610220  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington

Query Match 22.7%; Score 5; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10220  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US96-10220-25

Query Match 22.7%; Score 5; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPV 13  
Db 1 AAPV 5

RESULT 5  
US-08-658-639-3  
Sequence 3, Application US/08658639  
Patent No. 5914238  
GENERAL INFORMATION:  
APPLICANT: KEESEE, SUSAN  
APPLICANT: OBAR, ROBERT  
APPLICANT: WU, YING-YE  
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Testa, Hurwitz & Thibault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,639  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MEYERS, THOMAS C  
REGISTRATION NUMBER: 36,989

REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-658-639-3

Query Match 22.7%; Score 5; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEAA 10  
Db 2 AEAA 6

RESULT 6  
US-08-944-604-3  
Sequence 3, Application US/08944604  
Patent No. 6218131  
GENERAL INFORMATION:  
APPLICANT: KEESEE, SUSAN  
APPLICANT: OBAR, ROBERT  
APPLICANT: WU, YING-YE  
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Testa, Hurwitz & Thibault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,604  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MEYERS, THOMAS C  
REGISTRATION NUMBER: 36,989  
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-944-604-3

Query Match 22.7%; Score 5; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEAA 10  
Db 1 AEAA 10

Db 2 AAAAA 6

RESULT 7  
US-08-176-500-15  
; Sequence 15, Application US/08176500  
; Patent No. 5498538  
; GENERAL INFORMATION:  
; APPLICANT: Kay, B. K.  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; FILING DATE:  
; APPLICATION NUMBER: US/08/013,416  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-143  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-176-500-15

Query Match 22.7%; Score 5; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAAAA 10  
Db 7 AAAAA 11

RESULT 8  
US-08-471-052A-15  
; Sequence 15, Application US/08471052A  
; Patent No. 5625033  
; GENERAL INFORMATION:  
; APPLICANT: Kay, B. K.  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; FILING DATE:  
; APPLICATION NUMBER: US/08/471,052A  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-179  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; US-08-381-960-9

Query Match 22.7%; Score 5; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,052A  
; FILING DATE: 06-JUNE-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-179  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-471-052A-15

Query Match 22.7%; Score 5; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAAAA 10  
Db 7 AAAAA 11

RESULT 9  
US-08-381-960-9  
; Sequence 9, Application US/08381960  
; Patent No. 5723287  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Improvements in or relating to  
; TITLE OF INVENTION: recombinant viruses  
; NUMBER OF SEQUENCES: 10  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,960  
; FILING DATE:  
; CLASSIFICATION: 514  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; US-08-381-960-9

Query Match 22.7%; Score 5; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAAP 11  
|||||  
Db 4 EAAP 8

## RESULT 10

US-08-189-331-15  
; Sequence 15, Application US/08189331  
; Patent No. 5747334

## GENERAL INFORMATION:

APPLICANT: Kay, B. K.

APPLICANT: Fowlkes, D. M.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents

NUMBER OF SEQUENCES: 186

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/189,331

FILING DATE: Concurrently herewith

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-155

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-189-331-15

OY 6 EAAP 10  
|||||  
Db 7 EAAP 11

Query Match 22.7%; Score 5; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 11

US-08-471-939-15

; Sequence 15, Application US/08471939

; Patent No. 5844076

GENERAL INFORMATION:

APPLICANT: Kay, B. K.

APPLICANT: Fowlkes, D. M.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,939

FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/013,416

FILING DATE: 01-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-143

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-471-939-15

OY 6 EAAP 10  
|||||  
Db 7 EAAP 11

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 12

US-08-471-800-15

; Sequence 15, Application US/08471800

; Patent No. 5852167

GENERAL INFORMATION:

APPLICANT: Kay, B. K.

APPLICANT: Fowlkes, D. M.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,800

FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/013,416

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-143

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-800-15

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEA4A 10  
|||||  
DB 7 AEA4A 11

RESULT 13  
US-08-471-068-15  
Sequence 15, Application US/08471068  
Patent No. 5948635  
GENERAL INFORMATION:  
APPLICANT: Kay, B. K.  
APPLICANT: Fowlkes, D. M.  
TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
NUMBER OF SEQUENCES: 186  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennile & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,068  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/189,331  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-068-15

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 AEA4A 10  
|||||

DB 7 AEA4A 11

RESULT 14  
US-08-630-645-24  
Sequence 24, Application US/08630645  
Patent No. 5948763  
GENERAL INFORMATION:  
APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,645  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-630-645-24

Query Match 22.7%; Score 5; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPVY 13  
|||||  
DB 5 AAPVY 9

RESULT 15  
PCT-US96-10220-24  
Sequence 24, Application PC/TUS9610220  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington

STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10220  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US96-10220-24

Query Match 22.7%; Score 5; DB 5; Length 12;  
Best local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPV 13  
Db 5 AAPV 9

Search completed: July 23, 2001, 16:56:52  
Job time: 269 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: July 23, 2001, 16:56:11 ; Search time 65.41 Seconds  
(Without alignments)  
20.390 Million cell updates/sec

Title: US-09-351-296-13

Perfect score: 22

Sequence: 1 TATKQAAAPVYESKRALEY 22

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 148088

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

A\_Geneseq\_0601:\*

1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT:\*  
2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT:\*  
3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT:\*  
4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT:\*  
5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT:\*  
6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT:\*  
7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT:\*  
8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT:\*  
9: /SID58/gcgdata/geneseq/geneseq/AA1988.DAT:\*  
10: /SID58/gcgdata/geneseq/geneseq/AA1989.DAT:\*  
11: /SID58/gcgdata/geneseq/geneseq/AA1990.DAT:\*  
12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT:\*  
13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT:\*  
14: /SID58/gcgdata/geneseq/geneseq/AA1993.DAT:\*  
15: /SID58/gcgdata/geneseq/geneseq/AA1994.DAT:\*  
16: /SID58/gcgdata/geneseq/geneseq/AA1995.DAT:\*  
17: /SID58/gcgdata/geneseq/geneseq/AA1996.DAT:\*  
18: /SID58/gcgdata/geneseq/geneseq/AA1997.DAT:\*  
19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT:\*  
20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT:\*  
21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT:\*  
22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	17	AA999903 Hepatitis C Virus
2	18	81.8	22	17	AA999906 Hepatitis C Virus
3	10	45.5	22	17	AA995548 Hepatitis C Virus
4	9	40.9	9	17	AA99321 Human leucocyte an
5	8	36.4	11	17	AA99276 Human leucocyte an
6	5	22.7	7	18	AA99250 Anti-prion peptide
7	5	22.7	8	21	AA997838 Neisserial conserv
8	5	22.7	9	19	AA994355 Breast cancer asso
9	5	22.7	11	17	AA996835 Human neurofilamen
10	5	22.7	12	15	AA991235 Part of pntPeny in
11	5	22.7	12	18	AA992549 Anti-prion peptide

12	5	22.7	13	19	AA998350 Apoptosis associat
13	5	22.7	15	21	AA9982047 MHC class II prote
14	5	22.7	15	21	AA9982059 MHC class II prote
15	5	22.7	15	21	AA9982062 MHC class II prote
16	5	22.7	15	21	AA9982063 MHC class II prote
17	5	22.7	15	21	AA9982073 MHC class II prote
18	5	22.7	15	21	AA9982073 MHC class II prote
19	5	22.7	15	21	AA9982073 MHC class II prote
20	5	22.7	15	21	AA9982073 MHC class II prote
21	5	22.7	15	21	AA9982073 MHC class II prote
22	5	22.7	15	21	AA9982073 MHC class II prote
23	5	22.7	15	21	AA9982073 MHC class II prote
24	5	22.7	15	21	AA9982073 MHC class II prote
25	5	22.7	15	21	AA9982073 MHC class II prote
26	5	22.7	15	21	AA9982073 MHC class II prote
27	5	22.7	15	21	AA9982073 MHC class II prote
28	5	22.7	15	21	AA9982073 MHC class II prote
29	5	22.7	15	21	AA9982073 MHC class II prote
30	5	22.7	15	21	AA9982073 MHC class II prote
31	5	22.7	15	21	AA9982073 MHC class II prote
32	5	22.7	15	21	AA9982073 MHC class II prote
33	5	22.7	15	21	AA9982073 MHC class II prote
34	5	22.7	15	21	AA9982073 MHC class II prote
35	5	22.7	15	21	AA9982073 MHC class II prote
36	5	22.7	15	21	AA9982073 MHC class II prote
37	5	22.7	15	21	AA9982073 MHC class II prote
38	5	22.7	15	21	AA9982073 MHC class II prote
39	5	22.7	15	21	AA9982073 MHC class II prote
40	5	22.7	15	21	AA9982073 MHC class II prote
41	5	22.7	15	21	AA9982073 MHC class II prote
42	5	22.7	15	21	AA9982073 MHC class II prote
43	5	22.7	15	21	AA9982073 MHC class II prote
44	5	22.7	15	21	AA9982073 MHC class II prote
45	5	22.7	15	21	AA9982073 MHC class II prote

#### ALIGNMENTS

RESULT 1	
AA999903	
ID	AA999903 standard; peptide: 22 AA.
XX	
AC	AA999903;
XX	
DT	23-APR-1997 (first entry)
XX	
DE	Hepatitis C Virus antigen peptide 13.
XX	
KW	HCV; immunologically reactive; antigen; epitope; screen; typing;
KW	antibody; immobilised.
XX	
OS	Hepatitis C Virus.
XX	
PN	EP726463-A2.
XX	
PD	14-AUG-1996.
XX	
PF	09-FEB-1996; 96EP-0101925.
XX	
PR	09-FEB-1995; 95DE-4004302.
XX	
PA	(BOEF) BOEHRINGER MANNHEIM GMBH.
XX	
PI	Schmitt U, Seidel C, Wlenhues-thelen U;
XX	
PP	WPI; 1996-364504/37.
XX	
PT	Antibody typing by sequential reaction with immobilised antigens -
PT	esp. using new hepatitis C virus peptide(s) as antigens
XX	
PS	Claim 9; Page 14; 22pp; German.
XX	

CC AAR9891-920 comprise at least one immunologically active region of  
CC hepatitis C virus (HCV), selected from amino acid sequences 384-414,  
CC 1738-1759, 2217-2236, 2402-2419 and 2345-2357. The peptides are  
CC used in a claimed method for typing antibodies in a liq. sample.  
CC Assays performed using the peptides as antigens, which corresp. to  
CC regions of high immunogenicity and variability, can be performed  
CC routinely using simple equipment to provide accurate HCV typing.  
CC AAR9901-06 are derived from amino acids 1738-1759 of the NS4-region  
CC of HCV.  
XX  
SQ Sequence 22 AA;

Query Match 100.0%; Score 22; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.2e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TATKQAEAAAPVESKRALEY 22  
|  
Db 1 tatkgaaapveskraleV 22

## RESULT 2

AAR9906  
ID AAR9906 standard; peptide; 22 AA.

AC AAR9906;

DT 23-APR-1997 (first entry)

DE Hepatitis C Virus antigen peptide 16.

KW HCV; immunologically reactive; antigen; epitope; screen; typing;  
antibody; immobilised.

OS Hepatitis C Virus.

PN EP726463-A2.

PD 14-AUG-1996.

PF 09-FEB-1996; 96EP-0101925.

PR 09-FEB-1995; 95DE-4004302.

PA (BOEF ) BOEHRINGER MANNHEIM GMBH.

PI Schmitt U, Seidel C, Wienhues-thelen U;

DR WPI; 1996-364504/37.

PT Antibody typing by sequential reaction with immobilised antigens -  
esp. using new hepatitis C virus peptide(s) as antigens

PS Claim 9; Page 14; 22pp; German.

CC AAR9891-920 comprise at least one immunologically active region of  
CC hepatitis C virus (HCV), selected from amino acid sequences 384-414,  
CC 1738-1759, 2217-2236, 2402-2419 and 2345-2357. The peptides are  
CC used in a claimed method for typing antibodies in a liq. sample.  
CC Assays performed using the peptides as antigens, which corresp. to  
CC regions of high immunogenicity and variability, can be performed  
CC routinely using simple equipment to provide accurate HCV typing.  
CC AAR9901-06 are derived from amino acids 1738-1759 of the NS4-region  
CC of HCV.  
XX  
SQ Sequence 22 AA;

Query Match 81.8%; Score 18; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TATKQAEAAAPVESKWR 18  
|  
Db 1 tatkgaaapveskwr 18

## RESULT 3

AAR9548  
ID AAR9548 standard; peptide; 22 AA.

AC AAR9548;

DT 26-SEP-1996 (first entry)

DE Hepatitis C Virus I Non-Structural protein 4 epitope.

KW HCV; hepatitis C virus; epitope; antigen; detection; chimera.

OS Hepatitis C virus.

PN JP08073497-A.

PD 19-MAR-1996.

PF 31-AUG-1994; 94JP-0232073.

PR 31-AUG-1994; 94JP-0232073.

PA (TOFU ) TONEN CORP.

DR WPI; 1996-205533/21.

PT New hepatitis C virus chimeric antigenic peptide - for the detection  
of hepatitis C virus infection or its group

PS Claim 4; Page 14; 15pp; Japanese.

CC The present sequence is that of a group I hepatitis C virus (HCV)  
CC non-structural protein 4 (NS4) epitope, designated 1-Y. Chimeras  
CC prepared by connecting at least two different epitopes on the group I  
CC HCV-related antigen, encoded by the genomic RNA of HCV or its cDNA,  
CC through a peptide linkage, are useful for the specific detection of  
CC HCV infection.  
XX  
SQ Sequence 22 AA;

Query Match 45.5%; Score 10; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.0036;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TATKQAEAAA 10  
|  
Db 13 tatkgaaaaa 22

## RESULT 4

AAW49321  
ID AAW49321 standard; peptide; 9 AA.

AC AAW49321;

DT 05-JUN-1998 (first entry)

DE Human leucocyte antigen DQ4 binding peptide #212.

KW Human leucocyte antigen; HLA-DQ4; combinatorial library;  
autoimmune disease; chronic articular rheumatism.

OS Synthetic.

PN JP08151396-A.

PD 11-JUN-1996.



XX 28-NOV-1994; 94JP-0292657.  
PF Best Local Similarity 100.0%; Score 9; DB 17; Length 9;  
XX 28-NOV-1994; 94JP-0292657.  
PR Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX (TEIJ ) TEIJUN LTD.  
PA WPI: 1996-329479/33.  
XX  
DR HLA-binding oligopeptide and an immuno:regulator contg it - used in  
XX the treatment of auto:immune disease  
PT Claim 4; Page 30; 61pp; Japanese.  
XX  
PS This peptide is an example of a peptide which binds to a human leucocyte  
CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid  
CC combinatorial library comprising the sequence AAV05953, by screening  
CC with an HLA-DQ4 molecule. The peptide is used for the treatment of  
CC autoimmune disease, or especially for treatment of viral diseases.  
XX  
SQ Sequence 9 AA:  
  
Query Match 40.9%; Score 9; DB 17; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 APVYESKWR 18  
DB 1 apvyeskwr 9  
  
RESULT 5  
AAW49276  
ID AAW49276 standard; peptide; 11 AA.  
XX  
AC AAW49276;  
XX  
DF 05-JUN-1998 (first entry)  
XX  
DE Human leucocyte antigen DQ4 binding peptide #167.  
XX  
KW Human leucocyte antigen; HLA-DQ4; combinatorial library;  
KW autoimmune disease; chronic articular rheumatism.  
XX  
OS Synthetic.  
XX  
PN JP08151396-A.  
XX  
PD 11-JUN-1996.  
XX  
PF 28-NOV-1994; 94JP-0292657.  
XX  
PR 28-NOV-1994; 94JP-0292657.  
XX  
PA (TEIJ ) TEIJUN LTD.  
XX  
XX WPI: 1996-329479/33.  
XX  
DR HLA-binding oligopeptide and an immuno:regulator contg it - used in  
XX the treatment of auto:immune disease  
PT Claim 4; Page 26; 61pp; Japanese.  
XX  
PS This peptide is an example of a peptide which binds to a human leucocyte  
CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid  
CC combinatorial library comprising the sequence AAV05953, by screening  
CC with an HLA-DQ4 molecule. The peptide is used for the treatment of  
CC autoimmune disease, or especially for treatment of viral diseases.  
XX  
SQ Sequence 11 AA:

Query Match 36.4%; Score 8; DB 17; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 AAPVYES 15  
DB 1 aaapvyes 8  
  
RESULT 6  
AAW32550  
ID AAW32550 standard; peptide; 7 AA.  
XX  
AC AAW32550;  
XX  
DF 21-JAN-1998 (first entry)  
XX  
DE Anti-prion peptide inhibiting abnormal protein folding.  
XX  
KW Anti-amyloid peptide; IAbeta; abnormal protein folding inhibitor;  
KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;  
KW human prion disease; Kuru; Creutzfeldt-Jakob disease;  
KW Gerstmann-Strausler-Scheinker Syndrome; animal prion disease;  
KW prion associated human neurodegenerative disease; scrapie;  
KW spongiform encephalopathy; transmissible mink encephalopathy;  
KW chronic wasting disease; mule; deer; elk; human.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO9639834-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US10220.  
XX  
PR 10-APR-1996; 96US-0630645.  
PR 07-JUN-1995; 95US-0478326.  
XX  
PA (UYN ) UNIV NEW YORK STATE.  
XX  
PI Baumann MH, Frangione B, Soto-Jara C;  
XX  
DR WPI: 1997-051637/05.  
XX  
XX New inhibitors of fibrillogenesis proteins or peptides - used for  
PT preventing, treating or detecting amyloidosis disorders such as  
PT Alzheimer's disease.  
XX  
PS Claim 15; Page 40; 63pp; English.  
XX  
XX A method has been developed for the prevention or treatment of a  
CC disorder or disease associated with the formation of amyloid or  
CC amyloid-like deposits, involving the abnormal folding of a protein  
CC or peptide. The method involves administering an inhibitory peptide  
CC which prevents the abnormal folding or which dissolves existing amyloid  
CC or amyloid-like deposits, where the peptide comprises a sequence of  
CC 3-15 amino acid residues and has a hydrophobic cluster of at least 3  
CC amino acids, where at least one of the 3 amino acids is a beta-sheet  
CC blocking amino acid residue selected from Pro, Gly, Asn and His. The  
CC present sequence represents a specifically claimed example of an anti-  
CC prion peptide which inhibits abnormal protein folding. The inhibitory  
CC peptide is capable of associating with a structural determinant on the  
CC protein or peptide to structurally block and inhibit the abnormal  
CC folding into amyloid or amyloid-like deposits. The method can be used  
CC for preventing, treating or detecting e.g. Alzheimer's dementia or  
CC disease, Down's syndrome, other amyloidosis disorders, human prion  
CC diseases such as Kuru, Creutzfeldt-Jakob disease, Gerstmann-Strausler-  
CC Scheinker Syndrome, prion associated human neurodegenerative diseases or  
CC animal prion diseases such as scrapie, spongiform encephalopathy,  
CC transmissible mink encephalopathy and chronic wasting disease of mule  
CC deer and elk.  
XX

SQ Sequence 7 AA:

Query Match 22.7%; Score 5; DB 18; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPVY 13  
      |||||  
DB 1 aapv 5

RESULT 7

AAB37838  
ID AAB37838 standard; Peptide: 8 AA.

XX AC AAB37838;

XX DT 26-FEB-2001 (first entry)

XX DE Neisserial conserved peptide #21.

XX KW Neisseria meningitidis; Neisseria gonorrhoeae; antibacterial;

XX KM gene therapy; conserved sequence.

XX OS Neisseria sp.

XX PN WO20006741-A2.

XX PD 09-NOV-2000.

XX PF 28-APR-2000; 2000WO-IB00642.

XX PR 30-APR-1999; 99GB-0010168.

XX PR 09-MAR-2000; 2000GB-0005728.

XX PA (CHIR-) CHIRON SPA.

XX PI Rappunli R;

XX DR WPI; 2000-687543/67.

XX PT Novel Neisserial protein fragments and their corresponding nucleic  
XX acids, useful in the manufacture of medicines for the prevention of  
XX PT Neisserial infection, and in the manufacture of diagnostic reagents -  
XX PS Claim 15; Page 57; 157pp; English.

XX CC The present peptide is a conserved region of a Neisserial protein.  
XX CC Neisserial proteins containing this sequence, and the nucleic acids  
XX CC that encode such proteins, are useful in the manufacture of medicines  
XX CC for the prevention of Neisserial infection, and in the manufacture of  
XX CC multi-specific diagnostic reagents.

SQ Sequence 8 AA:

Query Match 22.7%; Score 5; DB 21; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPVY 13  
      |||||  
DB 4 aapv 8

RESULT 8

AAM44355  
ID AAM44355 standard; peptide: 9 AA.

XX AC AAM44355;

XX DT 28-MAY-1998 (first entry)

XX DE Breast cancer-associated protein fragment BC-2 SPQ ID NO:3.  
XX KW Human; breast cancer-associated protein; nuclear matrix protein;  
XX KM detection; diagnosis; antibody.

XX OS Homo sapiens.

XX PN WO9746884-A1.

XX PD 11-DEC-1997.

XX PF 03-JUN-1997; 97WO-US09529.

XX PR 05-JUN-1996; 96US-0658639.

XX PA (MATR-) MATRITECH INC.

XX PI Keesee SK, Obar R, Wu Y;

XX DR WPI; 1998-042336/04.

XX PT Diagnosing breast cancer by detecting a breast cancer-associated  
XX PT protein - allows early and reliable diagnosis and treatment  
XX PT monitoring, and antibody or inhibitory compounds useful for treating  
XX PT breast cancer

XX PS Claim 6; Page 29; 47pp; English.

XX CC The present sequence represents a breast cancer-associated protein  
XX CC fragment for use in a method for diagnosing breast cancer in tissue  
XX CC or body fluid by detecting one or more breast cancer-associated  
XX CC protein(s). Alternatively a nucleic acid encoding a breast cancer-  
XX CC associated protein is detected in the sample by the use of a nucleic  
XX CC acid probe. The breast cancer-associated proteins, encoding nucleic  
XX CC acids and antibodies are useful in diagnostic assays and kits for  
XX CC breast cancer detection. The proteins are also useful in screening for  
XX CC inhibitory compounds and monitoring effectiveness of treatments. The  
XX CC antibody, or pharmaceutical compositions containing the antibody or  
XX CC the inhibitory compound, can be administered to patients to treat  
XX CC breast cancer. The methods allow reliable and early diagnosis of  
XX CC breast cancer, or prediction of its onset, by detection of specific  
XX CC markers expressed in breast tumour cells but not in non-cancerous  
XX CC breast cells.

SQ Sequence 9 AA:

Query Match 22.7%; Score 5; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAAAA 10  
      |||||  
DB 2 aaaaa 6

RESULT 9

AAR96835  
ID AAR96835 standard; peptide: 11 AA.

XX AC AAR96835;

XX DT 29-NOV-1996 (first entry)

XX DE Human neurofilament triplet h fragment, homologous to Neisseria Iga-  
XX DE alphaI.

XX KW Iga protease precursor; IPP; bacterial polyprotein; autoimmune;  
XX KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;  
XX KW human neurofilament triplet h protein; Nfh; Neisseria gonorrhoeae;  
XX KW MS11.

```

OS Homo sapiens.
XX Key Location/Qualifiers
FH Region 1..3
FT /note= "identical to sequence in Neisseria gonorrhoeae
FT Region 5..7
FT /note= "identical to sequence in Neisseria gonorrhoeae
FT Region 10..11
FT /note= "identical to sequence in Neisseria gonorrhoeae
FT Iga-alpha1
XX WO9609395-A2.
XX 28-MAR-1996.
XX 21-SEP-1995; 95MO-EP03726.
XX 21-SEP-1994; 94DE-4433708.
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX Beck SC, Jose J, Lorenzen DR, Meyer TFF, Oetzelberger KB;
XX Pohlner J, Woelk U;
XX WPI; 1996-188456/19.
XX Medicaments for treating auto-immune or viral diseases - contg.
XX PT substances interfering with bacterial polyprotein function
XX PS Claim 32; Fig 2; 117pp; German.
XX CC The present sequence from human neurofilament triplet h protein has
XX CC homology to a cleavage product from the Iga-alpha1 domain of the
XX CC precursor of Iga-protease polyprotein (IPP) of Neisseria gonorrhoeae
XX CC strain MS11. The Neisseria IPP has been implicated in rheumatoid
XX CC arthritis and other auto-immune diseases. The polyprotein also
XX CC activates proviruses, including HIV. Substances which interfere with
XX CC the function of IPP from Neisseria will be useful for treating
XX CC associated autoimmune diseases and viral infections. Peptides
XX CC comprising the homology region sequences, whether from Neisseria or
XX CC from humans, are claimed.
XX SQ Sequence 11 AA;

Query Match 22.7%; Score 5; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEAHA 10
DB 7 aaaaa 11

RESULT 10
AAR51235 standard; Protein; 12 AA.
XX AAR51235;
XX 25-OCT-1994 (first entry)
XX Part of pNIPenv including a functional Bl.8scFv antibody.
XX Moloney murine leukaemia virus; Bl.8scFv antibody;
XX Bl.8scFv antibody.
XX Moloney murine leukaemia virus; Bl.8scFv antibody.
XX Chimeric MoJoney murine leukaemia virus.
XX Chimeric Mus musculus.
XX Key Location/Qualifiers

```

```

FT Peptide 1..7
FT /label= part of Bl.8scFv antibody
XX MO9406920-A.
XX 31-MAR-1994.
XX 22-SEP-1993; 93MO-GB01992.
XX 22-SEP-1992; 92GB-0020010.
XX 11-MAR-1993; 93GB-0004962.
XX (MEDI-) MEDICAL RES COUNCIL.
XX Hawkins RE, Russell SJ, Winter GP;
XX WPI; 1994-118469/14.
XX N-PSDB; AA045194.
XX Recombinant virus particles displaying nonviral polypeptide on
XX PT the surface - able to infect eukaryotic cells, useful for
XX PT targeted gene therapy, e.g. of tumours
XX Example 1; Page 64; 78pp; English.
XX AAR51235 shows the second part of the amino acid sequence of the
XX CC Bl.8-env fusion protein generated in pNIPenv. The first part
XX CC of the sequence is shown in AAR51234. Recombinant retroviruses
XX CC expressed a functional surface Bl.8 single chain Ab.
XX CC Ab fragments on the surface of recombinant retroviral particles
XX CC could be used to target virus to cells for gene delivery, or to
XX CC retain the virus in target tissues, or for the construction of
XX CC libraries of viral display packages.
XX SQ Sequence 12 AA;

Query Match 22.7%; Score 5; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EAAP 11
DB 4 eaap 8

RESULT 11
AAW32549
ID AAW32549 standard; peptide; 12 AA.
XX AAW32549;
XX 21-JAN-1998 (first entry)
XX Anti-prion peptide inhibiting abnormal protein folding.
XX Anti-amyloid peptide; Iabeta; abnormal protein folding inhibitor;
XX KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;
XX KW human prion disease; Kuru; Creutzfeldt-Jakob disease;
XX KW Gerstmann-Strausler-Scheinker Syndrome; animal prion disease;
XX KW prion associated human neurodegenerative disease; scrapie;
XX KW spongiform encephalopathy; transmissible mink encephalopathy;
XX KW chronic wasting disease; mule; deer; elk; human.
XX Homo sapiens.
XX Synthetic.
XX MO9639834-A1.
XX 19-DEC-1996.
XX 06-JUN-1996; 96MO-US10220.
XX

```

PR 10-APR-1996; 96US-0630645.  
PR 07-JUN-1995; 95US-0478326.  
XX  
PA (UNYNY ) UNIV NEW YORK STATE.  
PI Baumann MH, Frangione B, Soto-Jara C;  
XX WPI; 1997-051637/05.  
DR  
XX  
XX New inhibitors of fibrillogenesis proteins or peptides - used for  
PT preventing, treating or detecting amyloidosis disorders such as  
PT Alzheimer's disease.  
XX  
XX  
PS Claim 15; Page 40; 63pp; English.  
PS  
XX A method has been developed for the prevention or treatment of a  
CC disorder or disease associated with the formation of amyloid or  
CC amyloid-like deposits, involving the abnormal folding of a protein  
CC or peptide. The method involves administering an inhibitory peptide  
CC which prevents the abnormal folding or which dissolves existing amyloid  
CC or amyloid-like deposits, where the peptide comprises a sequence of  
CC 3-15 amino acid residues and has a hydrophobic cluster of at least 3  
CC amino acids, where at least one of the 3 amino acids is a beta-sheet  
CC blocking amino acid residue selected from Pro, Gly, Asn and His. The  
CC present sequence represents a specifically claimed example of an anti-  
CC prion peptide which inhibits abnormal protein folding. The inhibitory  
CC peptide is capable of associating with a structural determinant on the  
CC protein or peptide to structurally block and inhibit the abnormal  
CC folding into amyloid or amyloid-like deposits. The method can be used  
CC for preventing, treating or detecting e.g. Alzheimer's dementia or  
CC disease, Down's syndrome, other amyloidosis disorders, human prion  
CC diseases such as Kuru, Creutzfeldt-Jakob disease, Gerstmann-Strausler-  
CC Scheinker Syndrome, prion associated human neurodegenerative diseases or  
CC animal prion diseases such as scrapie, spongiform encephalopathy,  
CC transmissible mink encephalopathy and chronic wasting disease of mule  
CC deer and elk.  
XX  
XX  
SQ Sequence 12 AA;

Query Match 22.7%; Score 5; DB 18; Length 12;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AAPV 13  
| | | | |  
Db 5 aapv 9

RESULT 12  
AAW38350  
ID AAW38350 standard; Peptide: 13 AA.  
XX  
XX AAW38350;  
AC  
XX  
XX 08-JUN-1998 (first entry)  
DT  
XX  
XX Apoptosis associated protein Bbk BH3 domain mutant PM-IVLEE.  
DE  
XX  
XX Apoptosis associated protein; Bbk; BH3 domain; human; cell death;  
KW cell proliferation; degenerative disorder; gene therapy;  
KW Alzheimer's disease; autoimmune disease; cancer; inflammation.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX W09745128-A1.  
PN  
XX  
XX 04-DEC-1997.  
PD  
XX  
XX 29-MAY-1997; 97WO-US09194.  
PF  
XX  
XX 29-MAY-1996; 96US-0632514.  
PR

XX  
XX (APOP-) APOPTOSIS TECHNOLOGY INC.  
PA  
XX  
XX Gallo GJ;  
PI  
XX  
XX WPI; 1998-032326/03.  
DR  
XX  
XX  
XX Human apoptosis associated protein Bbk - useful to treat  
PT degenerative disorders characterised by inappropriate cell death or  
PT proliferation  
PT  
XX  
XX Example 8; Fig 9B; 110pp; English.  
PS  
XX  
XX This peptide comprises alanine scanning mutant PM-IVLEE of the BH3  
CC domain (see AAW38346) of human Bbk (see AAW38358), a novel apoptosis  
CC associated protein that can induce apoptosis in cells. PM-IVLEE  
CC contains 5 alanine substitutions in the BH3 element. It has  
CC completely lost BH3's apoptosis induction capabilities, supporting  
CC the conclusion that the BH3 region is absolutely necessary for  
CC Bbk's apoptotic function. Bbk and its BH3 domain can be used to  
CC treat degenerative disorders characterised by inappropriate cell  
CC death or proliferation.  
XX  
XX  
SQ Sequence 13 AA;

Query Match 22.7%; Score 5; DB 19; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1,1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEAA 10  
| | | | |  
Db 8 aaaa 12

RESULT 13  
AAW82047  
ID AAW82047 standard; peptide; 15 AA.  
XX  
XX AAW82047;  
AC  
XX  
XX 01-JUN-2000 (first entry)  
DT  
XX  
XX MHC class II protein binding peptide SEQ ID NO:15.  
DE  
XX  
XX MHC class II; major histocompatibility complex; autoimmune disease;  
KW inflammatory disease; binding; rheumatoid arthritis; antiinflammatory;  
KW antiarthritic; multiple sclerosis.  
XX  
XX  
XX Synthetic.  
OS  
XX  
XX W0200005249-A2.  
PN  
XX  
XX 03-FEB-2000.  
PD  
XX  
XX 22-JUL-1999; 99WO-US16617.  
PF  
XX  
XX 23-JUL-1998; 98US-0093859.  
PR  
XX  
XX 09-MAR-1999; 99US-0123675.  
PR  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX  
XX Strominger JL, Fridkis-Hareli M;  
PI  
XX  
XX WPI; 2000-205374/18.  
DR  
XX  
XX New synthetic peptide, useful for treating autoimmune disease, e.g.  
PT rheumatoid arthritis -  
PT  
XX  
XX Claim 22; Page 40; 57pp; English.  
PS  
XX  
XX The present invention describes synthetic peptides having an amino acid  
CC sequence comprising at least 3 residues selected from the group of amino  
CC

CC acids consisting of aromatic acids, negatively charged amino acids,  
CC positively charged amino acids, and aliphatic amino acids, the synthetic  
CC peptides being at least 7 amino acid residues in length and capable of  
CC binding to a major histocompatibility complex (MHC) class II protein  
CC associated with an autoimmune disease. The synthetic peptides have  
CC anti-inflammatory and anti-arthritic activities. They are used to treat  
CC rheumatoid arthritis and demyelinating autoimmune diseases, especially  
CC for particular MHC class II alleles. Purified, short and synthetic  
CC peptides should have fewer side effects than mixtures of random  
CC peptides; may include many repeats of the active sequence and/or contain  
CC amino acid analogues that improve stability (or other desired features).  
CC AAY82021 to AAY82044 represent specifically claimed peptide sequences  
CC which can be used as part of the synthetic peptides of the present  
CC invention. AAY82045 to AAY82063 represent specifically claimed examples  
CC of the synthetic peptides from the present invention; and AAY82064 to  
CC AAY82080 represent other peptides used in the exemplification of the  
CC present invention.  
SQ Sequence 15 AA;

Query Match 22.7%; Score 5; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAAAA 10  
|||||  
DB 5 aaaaa 9

## RESULT 14

ID AAY82059 standard; peptide: 15 AA.

XX AAY82059;

DT 01-JUN-2000 (first entry)

DE MHC class II protein binding peptide SEQ ID NO:29.

XX MHC class II; major histocompatibility complex; autoimmune disease;  
KW inflammatory disease; binding; rheumatoid arthritis; antiinflammatory;  
KW antiarthritic; multiple sclerosis.

OS Synthetic.

PN WO200005249-A2.

PD 03-FEB-2000.

PF 22-JUL-1999; 99WO-US16617.

PR 23-JUL-1998; 98US-0093859.

PR 09-MAR-1999; 99US-0123675.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Harell M;

DR WPI; 2000-205374/18.

PT New synthetic peptide, useful for treating autoimmune disease, e.g.

PT rheumatoid arthritis -

PS Claim 24; Page 41; 57pp; English.

XX The present invention describes synthetic peptides having an amino acid  
CC sequence comprising at least 3 residues selected from the group of amino  
CC acids consisting of aromatic acids, negatively charged amino acids,  
CC positively charged amino acids, and aliphatic amino acids, the synthetic  
CC peptides being at least 7 amino acid residues in length and capable of  
CC binding to a major histocompatibility complex (MHC) class II protein

CC associated with an autoimmune disease. The synthetic peptides have  
CC anti-inflammatory and anti-arthritic activities. They are used to treat  
CC inflammatory and demyelinating autoimmune diseases, especially  
CC rheumatoid arthritis and multiple sclerosis. The peptides are specific  
CC for particular MHC class II alleles. Purified, short and synthetic  
CC peptides should have fewer side effects than mixtures of random  
CC peptides; may include many repeats of the active sequence and/or contain  
CC amino acid analogues that improve stability (or other desired features).  
CC AAY82021 to AAY82044 represent specifically claimed peptide sequences  
CC which can be used as part of the synthetic peptides of the present  
CC invention. AAY82045 to AAY82063 represent specifically claimed examples  
CC of the synthetic peptides from the present invention; and AAY82064 to  
CC AAY82080 represent other peptides used in the exemplification of the  
CC present invention.  
SQ Sequence 15 AA;

Query Match 22.7%; Score 5; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAAAA 10  
|||||  
DB 5 aaaaa 9

## RESULT 15

ID AAY82062 standard; peptide: 15 AA.

XX AAY82062;

DT 01-JUN-2000 (first entry)

DE MHC class II protein binding peptide SEQ ID NO:35.

XX MHC class II; major histocompatibility complex; autoimmune disease;  
KW inflammatory disease; binding; rheumatoid arthritis; antiinflammatory;  
KW antiarthritic; multiple sclerosis.

OS Synthetic.

PN WO200005249-A2.

PD 03-FEB-2000.

PF 22-JUL-1999; 99WO-US16617.

PR 23-JUL-1998; 98US-0093859.

PR 09-MAR-1999; 99US-0123675.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Harell M;

DR WPI; 2000-205374/18.

PT New synthetic peptide, useful for treating autoimmune disease, e.g.

PT rheumatoid arthritis -

PS Claim 24; Page 41; 57pp; English.

XX The present invention describes synthetic peptides having an amino acid  
CC sequence comprising at least 3 residues selected from the group of amino  
CC acids consisting of aromatic acids, negatively charged amino acids,  
CC positively charged amino acids, and aliphatic amino acids, the synthetic  
CC peptides being at least 7 amino acid residues in length and capable of  
CC binding to a major histocompatibility complex (MHC) class II protein  
CC associated with an autoimmune disease. The synthetic peptides have  
CC anti-inflammatory and anti-arthritic activities. They are used to treat  
CC inflammatory and demyelinating autoimmune diseases, especially  
CC rheumatoid arthritis and multiple sclerosis. The peptides are specific

CC for particular MHC Class II alleles. Purified, short and synthetic  
CC peptides should have fewer side effects than mixtures of random  
CC peptides; may include many repeats of the active sequence and/or contain  
CC amino acid analogues that improve stability (or other desired features).  
CC AY82021 to AY82044 represent specifically claimed peptide sequences  
CC which can be used as part of the synthetic peptides of the present  
CC invention; AY82045 to AY82063 represent specifically claimed examples  
CC of the synthetic peptides from the present invention; and AY82064 to  
CC AY82080 represent other peptides used in the exemplification of the  
CC present invention.

XX  
SQ Sequence 15 AA;

Query Match 22.7%; Score 5; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEAAA 10  
| | | | |  
DB 4 aaaaa 8

Search completed: July 23, 2001, 16:56:12  
Job time: 529 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:56:59 ; Search time 69.82 Seconds  
(Without alignments)  
41.689 Million cell updates/sec

Title: US-09-351-296-12

Perfect score: 22  
Sequence: 1 TASHRAEVTTPAVQTNMCKLEY 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5654

Minimum DB seq length: 6  
Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_16:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.unclassified:\*  
13: sp.vertebrate:\*  
14: sp.virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5	22.7	20	8	095947	095947 saccharomyc
2	4	18.2	12	6	09TR63	09TR63 sus scrofa
3	4	18.2	15	3	09UR90	09UR90 saccharomyc
4	4	18.2	16	3	09URB8	09URB8 saccharomyc
5	4	18.2	16	4	09UCR9	09UCR9 homo sapien
6	4	18.2	19	8	09ZYW1	09ZYW1 histomeru
7	4	18.2	20	4	016188	016188 homo sapien
8	4	18.2	21	2	09R4T3	09R4T3 mycobacteri
9	3	13.6	8	2	068485	068485 Klebsiella
10	3	13.6	8	11	062933	062933 rattus norv
11	3	13.6	9	2	P82568	P82568 streptococ
12	3	13.6	9	11	088889	088889 mus musculu
13	3	13.6	10	4	09UCS3	09UCS3 homo sapien
14	3	13.6	10	11	070580	070580 mus musculu
15	3	13.6	10	11	063389	063389 rattus norv
16	3	13.6	11	2	056413	056413 escherichia
17	3	13.6	11	4	09UBM2	09UBM2 homo sapien
18	3	13.6	12	2	056442	056442 unidentified
19	3	13.6	12	2	09X6Y0	09X6Y0 aquifex pyr

20	3	13.6	12	2	052112	052112 actinobact
21	3	13.6	12	4	09UC37	09UC37 homo sapien
22	3	13.6	12	10	041856	041856 zea mays (m
23	3	13.6	12	10	09S0F8	09S0F8 pinus laeda
24	3	13.6	12	10	P82334	P82334 pisum sativ
25	3	13.6	12	14	09IF00	09IF00 human adeno
26	3	13.6	12	14	09IEZ9	09IEZ9 human adeno
27	3	13.6	13	2	09R8R9	09R8R9 streptococ
28	3	13.6	13	2	P82560	P82560 streptococ
29	3	13.6	13	5	09U7D6	09U7D6 toxoplasma
30	3	13.6	13	5	09U7D6	09U7D6 neospora ca
31	3	13.6	13	11	060517	060517 mus musculu
32	3	13.6	13	14	081770	081770 hepatitis c
33	3	13.6	14	2	047599	047599 escherichia
34	3	13.6	14	2	09X715	09X715 campylobact
35	3	13.6	14	2	09X715	09X715 bacillus ha
36	3	13.6	14	6	09XSL4	09XSL4 capra hircu
37	3	13.6	14	14	085622	085622 reovirus sp
38	3	13.6	14	14	056127	056127 porcine citr
39	3	13.6	14	14	086616	086616 turkey heip
40	3	13.6	14	14	093202	093202 porcine citr
41	3	13.6	15	2	068430	068430 buchnera ap
42	3	13.6	15	2	046456	046456 clostridium
43	3	13.6	15	2	047892	047892 fremyella d
44	3	13.6	15	2	09R563	09R563 escherichia
45	3	13.6	15	2	09R531	09R531 thermus. ch

## ALIGNMENTS

RESULT 1  
ID 095947 PRELIMINARY; PRT; 20 AA.  
AC 095947;  
DT 01-FEB-1997 (TREMREL. 02, Created)  
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)  
DT 01-MAY-2000 (TREMREL. 13, Last annotation update)  
DE MITOCHONDRIAL CYTOCHROME OXIDASE SUBUNIT I (EC 1.9.3.1) (FRAGMENT).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Novitski C.E., Macreadie I.G., Maxwell R.J., Lukins H.B.,  
RA Linanne A.W., Nagley P.;  
RL Curr. Genet. 8:135-146(1984).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85035872; PubMed=6387398;  
RA Simon M., Faye G.;  
RT "Organization and processing of the mitochondrial ox13/ol12 multigenic  
RT transcript in yeast.";  
RT Mol. Genet. 196:266-274(1984).  
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4  
CC -1- FERRICYTOCHROME C.  
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.  
DR EMBL: M36379; AAA32147.1; -;  
DR EMBL: X00960; CA25472.1; -;  
DR Mitochondrion; Oxidoreductase; Heme; Copper; Transmembrane;  
KW Respiratory chain.  
FT NON\_TER 1  
SQ SEQUENCE 20 AA; 2142 MW; AAF7B024CD94F2D6 CRC64;

Query Match 22.7%; Score 5; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 TPAVO 14

Db 15 TPAVO 19

RESULT 2

Q9TTE3 ID Q9TTE3 PRELIMINARY; PRT; 12 AA.  
AC Q9TTE3; DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE GLUTATHIONE PEROXIDASE 5 (FRAGMENT).  
GN GPX5.  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bertani G.R., Marklund S., Hu Z.L., Rothschild M.F.;  
RT "Mapping of the glutathione peroxidase 5 (GPX5) gene to pig chromosome 7.";  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
KW Peroxidase.  
DR EMBL; AF124818; AAF22118.1; -.  
FT NON\_TER 1 1  
FT 12 12  
SQ SEQUENCE 12 AA; 1307 MW; D4E39EEF50B451B6 CRC64;

Query Match 18.2%; Score 4; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VQTN 16  
Db 4 VQTN 7

RESULT 3

Q9UR90 ID Q9UR90 PRELIMINARY; PRT; 15 AA.  
AC Q9UR90; DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE CYCLOPHILIN A (FRAGMENT).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=93278320; PubMed=1304384;  
RA Zydowsky L.D., Ho S.I., Baker C.H., McIntyre K., Walsh C.T.;  
RT "Overexpression, purification, and characterization of yeast RT cyclophilins A and B.";  
RL Protein Sci. 1:961-969(1992).  
SQ SEQUENCE 15 AA; 1648 MW; 9FD36B8DC370A405 CRC64;

Query Match 18.2%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EVIT 10  
Db 12 EVIT 15

RESULT 4  
Q9URB8 ID Q9URB8 PRELIMINARY; PRT; 16 AA.

AC Q9URB8; DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CYCLOPHILIN-RELATED PROTEIN, CYP-RELATED PROTEIN.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92087095; PubMed=1721297;  
RA Tanida I., Yanagida M., Maki N., Yagi S., Namiyama F., Kobayashi T.,  
RA Hayano T., Takahashi N., Suzuki M.;  
RT "Yeast cyclophilin-related gene encodes a nonessential second RT peptidyl-prolyl cis-trans isomerase associated with the secretory RT pathway.";  
RL Transplant. Proc. 23:2856-2861(1991).  
SQ SEQUENCE 16 AA; 1776 MW; 715FD36B8DC370A4 CRC64;

Query Match 18.2%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EVIT 10  
Db 12 EVIT 15

RESULT 5

Q9UCK9 ID Q9UCK9 PRELIMINARY; PRT; 16 AA.  
AC Q9UCK9; DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE SERUM AMYLOID A ISOTYPE 2 ALPHA PROTEIN (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93099171; PubMed=1463770;  
RA Baba S., Takahashi T., Kasama T., Shirasawa H.;  
RT "Identification of two novel amyloid A protein subsets coexisting in RT an individual patient of AA-amyloidosis.";  
RL Biochim. Biophys. Acta 1180:195-200(1992).  
DR InterPro: IPR000096; -.  
DR Pfam: PF00277; SAA\_proteins; 1.  
SQ SEQUENCE 16 AA; 1612 MW; 1CAB4F077C9C8C1 CRC64;

Query Match 18.2%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AEVI 9  
Db 9 AEVI 12

RESULT 6  
Q92YWL ID Q92YWL PRELIMINARY; PRT; 19 AA.  
AC Q92YWL; DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
DE CYTOCHROME OXIDASE II (FRAGMENT).  
OS Histeromerus mystacinus.



OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;  
 OC Ichneumonidae; Braconidae; Doryctinae; Histeromerus.  
 ON NCBI\_TaxID=55923;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99152621; PubMed=10028295;  
 RA Dowton M., Austin A.D.;  
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in  
 the Hymenoptera."  
 RL MOL. BIOL. EVOL. 16:298-309(1999).  
 DR EMBL: AF034600; AAC79748.1; -.  
 KM Mitochondrion.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 19 AA: 2345 MW: 366A2590E3D436CD CRC64;  
  
 Query Match 18.2%; Score 4; DB 8; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 19 KLEV 22  
 IIII  
 Db 7 KLEV 10  
  
 RESULT 7  
 Q16188 PRELIMINARY; PRT; 20 AA.  
 AC 016188;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
 DE ADENOSINE DEAMINASE PROTEIN (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94327968; PubMed=8051429;  
 RA Shovlin C.L., Simmonds H.A., Fairbanks L.D., Deacock S.J.,  
 RA Hughes J.M., Lechler R.I., Webster A.D., Sun X.M., Webb J.C.,  
 RA Soutar A.K.;  
 RT "Adult onset immunodeficiency caused by inherited adenosine deaminase  
 deficiency."  
 RL J. Immunol. 153:2331-2339(1994).  
 DR EMBL: S72469; AAD14102.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 20 AA: 2175 MW: 4EAB6143F739B4C CRC64;  
  
 Query Match 18.2%; Score 4; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 8 VITP 11  
 IIII  
 Db 1 VITP 4  
  
 RESULT 8  
 Q9R4T3 PRELIMINARY; PRT; 21 AA.  
 AC 09R4T3;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE PYRIDINE NUCLEOTIDE TRANSHYDROGENASE (FRAGMENT).  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.

ON NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95122409; PubMed=7822223;  
 RA Deshpande R.G., Khan M.B., Bhat D.A., Navalkar R.G.;  
 RT "Isolation of a 43 kDa protein from Mycobacterium tuberculosis H37RV  
 and its identification as a pyridine nucleotide transhydrogenase."  
 RL J. Appl. Bacteriol. 77:639-643(1994).  
 SQ SEQUENCE 21 AA: 2358 MW: B425988639C2A9BA CRC64;  
  
 Query Match 18.2%; Score 4; DB 2; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 9 ITPA 12  
 IIII  
 Db 18 ITPA 21  
  
 RESULT 9  
 Q68485 PRELIMINARY; PRT; 8 AA.  
 AC 068485;  
 DT 01-AUG-1998 (TREMBlrel. 07, Created)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
 DE AMINOGLYCOSIDE 3'-O-NUCLEOTIDYLTRANSFERASE (FRAGMENT).  
 OS AADAI.  
 GN Klebsiella pneumoniae.  
 OC Plasmid pUQ100.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Klebsiella.  
 ON NCBI\_TaxID=573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KL;  
 RA Centron D., Roy P.H.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF047556; AAC25501.1; -.  
 KM Transferase; Plasmid.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA: 878 MW: EFC1B5A2CB1DD056 CRC64;  
  
 Query Match 13.6%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 AEV 8  
 IIII  
 Db 3 AEV 5  
  
 RESULT 10  
 Q62933 PRELIMINARY; PRT; 8 AA.  
 AC 062933;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
 DE HISTONE H10 (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WISTAR; TISSUE=TESTIS;  
 RA Knochlin S., Peretti M.F., Girardot V.;  
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U49737; AAA92724.1; -.  
 FT NON\_TER 8 8

SO SEQUENCE 8 AA; 850 MW; F4C71B5B44B01A6 CRC64;

Query Match 13.6%; Score 3; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 TPA 12  
|||  
Db 6 TPA 8

RESULT 11  
P82568 PRELIMINARY; PRT; 9 AA.

AC P82568;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE UNKNOWN PROTEIN FROM 2D-PAGE (FRAGMENT).  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
OC Streptococcus.  
NCBI\_TaxID=1314;

RN NCBI\_TaxID=1314;  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC STRAIN-JRS4;  
RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,  
RA VanBogelen R.A.;  
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes  
RT proteins.";  
RL Submitted (MAY-2000) to the SWISS-PROT data bank.  
CC -1- MASS SPECTROMETRY: MW=22592.04; METHOD=ELECTROSPRAY.  
FT NON\_TER 1 1  
FT NON\_TER 9 9

SO SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 EVI 9  
|||  
Db 5 EVI 7

RESULT 12  
O88889

ID O88889 PRELIMINARY; PRT; 9 AA.

AC O88889;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE UBIQUITIN-CONJUGATING ENZYME UBCM4 (FRAGMENT).  
GN UBCM4.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
NCBI\_TaxID=10090;

RN NCBI\_TaxID=10090;  
RP SEQUENCE FROM N.A.  
RC STRAIN-129/SV;  
RX MEDLINE=97057256; PubMed=8901595;  
RA Harbers K., Muller U., Grams A., Li E., Jaenisch R., Franz T.,  
RT "Provirus integration into a gene encoding a ubiquitin-conjugating  
RT enzyme results in a placental defect and embryonic lethality.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:12412-12417(1996).  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-129/SV;  
RA Mueller U., Grams A., Martinez-Noel G., Copeland N.G., Gilbert D.J.,  
RA Jenkins N.A., Harbers K.;

RT "Structure of the gene encoding the ubiquitin-conjugating enzyme  
RT UbcM4, characterization of its promoter and chromosomal location.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF071557; AAD10128.1; -.  
FT NON\_TER 9 9  
SO SEQUENCE 9 AA; 1063 MW; C90E97341415BDD CRC64;

Query Match 13.6%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASR 4  
|||  
Db 3 ASR 5

RESULT 13  
Q9UCS3 PRELIMINARY; PRT; 10 AA.

AC Q9UCS3;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE TROPOMYOSIN-3 KDA CALCIUM BINDING PROTEIN FRAGMENT D.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE.  
RX MEDLINE=92090441; PubMed=1836432;  
RA Cribos M., Yamakado T., Helzmann C.W., Cerletti N., Buhler F.R.,  
RA Erne P.;  
RT "The calcium binding protein tropomyosin in human platelets and  
RT cardiac tissue: elevation in hypertensive cardiac hypertrophy.";  
RL Eur. J. Clin. Invest. 21:472-478(1991).  
SO SEQUENCE 10 AA; 1126 MW; 7A44FD3DC2DAFAEB CRC64;

Query Match 13.6%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 KLE 21  
|||  
Db 8 KLE 10

RESULT 14  
O70580

ID O70580 PRELIMINARY; PRT; 10 AA.

AC O70580;  
DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
DE CARBONIC ANHYDRASE III (FRAGMENT).  
GN CA3.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
NCBI\_TaxID=10090;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Sowden J., Smith H., Morrison K., Edwards Y.,  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ006474; CAA07057.1; -.  
FT NON\_TER 10 10  
SO SEQUENCE 10 AA; 1105 MW; 56F7FE71ADC37B13 CRC64;

Query Match 13.6%; Score 3; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 10 TPA 12  
 |||  
 Db 7 TPA 9

## RESULT 15

063389 PRELIMINARY; PRT: 10 AA.  
 AC 063389;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)  
 DE ORNITHINE DECARBOXYLASE (ODC).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN |||  
 RP SEQUENCE FROM N. A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=TESTIS;  
 RX MEDLINE=89253378; PubMed=2722815;  
 RA Wen L., Huang J. K., Blackshear P. J.;  
 RT "Rat ornithine decarboxylase gene. Nucleotide sequence, potential  
 RT regulatory elements, and comparison to the mouse gene.";  
 RL J. Biol. Chem. 264:9016-9021(1989).  
 DR EMBL; J04791; AAA66163.1; -.  
 SQ SEQUENCE 10 AA; 1074 MW; 30F6E69D415BDC7 CRC64;

Query Match 13.6%; Score 3; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 ASR 4  
 |||  
 Db 4 ASR 6

Search completed: July 23, 2001, 17:06:05  
 Job time: 546 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:56:19 ; Search time 23.18 Seconds  
(without alignments)  
32.512 Million cell updates/sec

Title: US-09-351-296-12

Sequence: 1 TASRAHEVITPAVQTNMOKLEV 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1176

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	18.2	17	1 UN15_CLOPA	P81334 Clostridium
2	3	13.6	8	1 LPMS_STAEP	P23211 staphylococ
3	3	13.6	9	1 FABF_RHIME	P56902 rhizobium m
4	3	13.6	9	1 XYLA_STRSO	P19149 streptomyc
5	3	13.6	10	1 COXK_ONCMY	P60332 oncothymchu
6	3	13.6	10	1 UPAB_HUMAN	P30094 homo sapien
7	3	13.6	12	1 NO40_LORJA	O24246 lotus japon
8	3	13.6	12	1 NO40_SESRO	O24369 sesbania ro
9	3	13.6	12	1 TM2A_METMA	P80652 methanosarc
10	3	13.6	13	1 IDHA_CANFA	P54836 canis famill
11	3	13.6	13	1 NO40_PEA	P55959 pisum sativ
12	3	13.6	13	1 NO40_VITSA	P55961 vicia sativ
13	3	13.6	13	1 UVRD_SALTY	O05311 salmoneilla
14	3	13.6	15	1 COXJ_THUOB	P80979 thunnus obe
15	3	13.6	15	1 PDGB_PIG	P20034 sus scrofa
16	3	13.6	15	1 RM12_YEAST	P36522 saccharomyc
17	3	13.6	15	1 YAA3_RHOPA	O02006 rhodospseud
18	3	13.6	16	1 AMP8_ELEGR	P11921 eleginus gr
19	3	13.6	16	1 HTPG_ACICA	P81876 acinetobact
20	3	13.6	16	1 R1PK_TRIKI	P16093 trichosanth
21	3	13.6	17	1 ARGD_SALTY	P40732 salmoneilla
22	3	13.6	17	1 F1BA_PIG	P14460 sus scrofa
23	3	13.6	17	1 NEF_HV13	P12460 human immun
24	3	13.6	18	1 OBP_HYACE	P34173 hyalophora
25	3	13.6	18	1 OBP_LYMDI	P34173 lymantria d
26	3	13.6	19	1 AMY_DERPT	P49274 dermatophag
27	3	13.6	19	1 ANP7_ELEGR	P11920 eleginus gr
28	3	13.6	19	1 CH10_CLOPA	P81338 Clostridium
29	3	13.6	19	1 PA2S_HUMAN	P24606 homo sapien
30	3	13.6	19	1 PHSU_DESBN	P13066 desulfovibr
31	3	13.6	19	1 RECO_SALTY	P13066 salmoneilla
32	3	13.6	19	1 RL10_CITFR	P34448 citrobacter
33	3	13.6	19	1 TPIS_CLOPA	P81348 Clostridium

## ALIGNMENTS

34	3	13.6	20	1	ATP4_SPIOL	P80085 spinacia ol
35	3	13.6	20	1	CHP_THICH	P80486 thibacillu
36	3	13.6	20	1	DEP4_BOVIN	P81425 bos taurus
37	3	13.6	20	1	EMA2_MOUSE	P31230 mus musculu
38	3	13.6	20	1	JHBP_BOMMO	P81627 bombyx mori
39	3	13.6	20	1	RL10_PROVU	P51411 proteus vul
40	3	13.6	20	1	SODM_HORVU	P28524 bordetella
41	3	13.6	20	1	VR90_BORPE	P81549 bordetella
42	3	13.6	21	1	CXGT_CONTU	P17684 conus tulip
43	3	13.6	21	1	FEDB_AMEYE	P80706 amycolatops
44	3	13.6	21	1	GYRA_STRSH	P50071 streptomyc
45	3	13.6	21	1	ODP2_SOLTU	P81421 solanum tub

RESULT 1  
ID UN15\_CLOPA STANDARD; PRT: 17 AA.  
AC P81334;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE UNKNOWN PROTEIN CP 15 FROM 2D-PAGE (FRAGMENT).  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_Taxid=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flegensrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
RT sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -I- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.1, ITS MW IS: 38.9 KDA.  
FT NON\_TER  
SQ SEQUENCE 17 AA; 2015 MW; 46F8D8DC1A1CB4A CRC64;

Query Match 18.2%; Score 4; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 OKLE 21  
Db 4 OKLE 7

RESULT 2  
ID LPMS\_STAEP STANDARD; PRT: 8 AA.  
AC P23211;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-MAR-1992 (Rel. 21, Last annotation update)  
DE PROBABLE MSRA LEADER PEPTIDE.  
OS staphylococcus epidermidis.  
OC plasmid pU5050.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_Taxid=1282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=968;  
RX MEDLINE=91041730; PubMed=2233255;  
RA Ross J.I., Eady E.A., Cove J.H., Cunliffe W.J., Baumberg S.,  
RA Wootton J.C.;  
RT "Inducible erythromycin resistance in staphylococci is encoded by a  
member of the ATP-binding transport super-gene family.";

```

RL  Mol. Microbiol. 4:1207-1214(1990).
CC  -1- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE
CC  PROTEIN.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: X52085; CAA36303.1; -.
DR  PIR: S1157; LFSAME.
KW  Leader peptide; Plasmid.
SQ  SEQUENCE 8 AA; 937 MW; FA37340685BDC1A6 CRC64;

Query Match      13.6%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 TAS 3
    |||
DB  2 TAS 4

RESULT 3
FABF_RHIME STANDARD; PRT; 9 AA.
ID  FABF_RHIME
AC  P56902;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DE  30-MAY-2000 (Rel. 39, Last annotation update)
DE  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE II (EC 2.3.1.41) (BETA-
DE  KETOACYL-ACP SYNTHASE II) (KAS II) (FRAGMENT).
GN  FABF.
OS  Rhizobium meliloti (Sinorhizobium meliloti).
OC  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC  Rhizobiaceae; Sinorhizobium.
OX  NCBI_TaxID=382;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Lopez-Lara I.M., Geiger O.;
RC  STRAIN=1021;
RT  "Heterologous overexpression of different rhizobial acyl carrier
RT  proteins in Escherichia coli and their purification.";
RL  Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
CC  -1- FUNCTION: CATALYZES THE CONDENSATION REACTION OF FATTY ACID
CC  SYNTHESIS BY THE ADDITION TO AN ACYL ACCEPTOR OF TWO CARBONS
CC  FROM MALONYL-ACP. HAS A PREFERENCE FOR SHORT CHAIN ACID SUBSTRATES
CC  AND MAY FUNCTION TO SUPPLY THE OCTANOIC SUBSTRATES FOR LIPIDIC ACID
CC  BIOSYNTHESIS (BY SIMILARITY).
CC  -1- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + MALONYL-[ACYL-
CC  CARRIER PROTEIN] = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + CO(2) +
CC  [ACYL-CARRIER PROTEIN].
CC  -1- PATHWAY: FATTY ACID BIOSYNTHESIS.
CC  -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE BETA-KETOACYL-ACP SYNTHASES FAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: AF159244; AAF24182.1; -.
DR  InterPro: IPR000794; ...
DR  PROSITE: PS00606; B_KETOACYL_SYNTHASE; PARTIAL.
KW  Fatty acid biosynthesis; Transferase; Acyltransferase.
FT  NON_TER 9

```

```

SQ  SEQUENCE 9 AA; 1032 MW; 749161A042D2D414 CRC64;

Query Match      13.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 VIT 10
    |||
DB  5 VIT 7

RESULT 4
XYLA_STRSQ STANDARD; PRT; 9 AA.
ID  XYLA_STRSQ
AC  P19149;
DT  01-NOV-1990 (Rel. 16, Created)
DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  XYLOSE ISOMERASE (EC 5.3.1.5) (FRAGMENT).
OS  Streptomyces sp. (strain NCL 82-5-1).
OC  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC  Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX  NCBI_TaxID=1931;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=88326335; PubMed=1415697;
RA  Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;
RT  "Purification and characterisation of glucose (xylose) isomerase from
RT  Chaetia sp. (NCL 82-5-1).";
RL  Biochem. Biophys. Res. Commun. 155:411-417(1988).
CC  -1- FUNCTION: INVOLVED IN D-XYLOSE CATABOLISM.
CC  -1- CATALYTIC ACTIVITY: D-XYLOSE = D-XYLULOSE.
CC  -1- COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY.
CC  -1- SUBUNIT: HOMOTETRAMER.
CC  -1- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
CC  -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
DR  PIR: A31576; A31576.
DR  InterPro: IPR001998; ...
DR  PROSITE: PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
DR  PROSITE: PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
KW  Isomerase; Pentose shunt; Xylose metabolism; Magnesium.
FT  NON_TER 9
SQ  SEQUENCE 9 AA; 983 MW; F64BA1EDC5B87DD1 CRC64;

Query Match      13.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 RHA 6
    |||
DB  1 RHA 3

RESULT 5
COXK_ONCMY STANDARD; PRT; 10 AA.
ID  COXK_ONCMY
AC  P80332;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  01-OCT-2000 (Rel. 40, Last annotation update)
DE  CYTOCHROME C OXIDASE POLYPEPTIDE VITA-HEART (EC 1.9.3.1) (FRAGMENT).
OS  Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC  Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX  NCBI_TaxID=8022;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Heart;
RX  MEDLINE=94237150; PubMed=8181469;
RA  Freund R., Kadenbach B.;

```

RT "Identification of tissue-specific isoforms for subunits Vb and V1a of cytochrome c oxidase isolated from rainbow trout.";  
 RL Eur. J. Biochem. 221:1111-1116(1994).  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4 FERROCYTOCHROME C.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.  
 DR PIR: S43631; S43631.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1174 MW; 4C8DB1CAFAF772C3 CRC64;

Query Match 13.68; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 OKL 20  
 Db 8 OKL 10

## RESULT 6

UP8A\_HUMAN STANDARD; PRT; 10 AA.  
 AC P30094;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 34) (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravlier F., Pasquall C., Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B., Hochstrasser D.F.;  
 RA "Plasma protein map: an update by microsequencing.";  
 RL Electrophoresis 13:707-714(1992).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 7.2, ITS MW IS: 16 KDA.  
 DR SWISS-2DPAGE; P30094; HUMAN.  
 FT NON\_TER 1 1  
 FT VARIANT 4 4 S->H.  
 FT NON\_TER 10 10 /FTID=VAR\_000003.  
 SQ SEQUENCE 10 AA; 977 MW; 2EA6E0C77AE325B8 CRC64;

Query Match 13.68; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 PAV 13  
 Db 7 PAV 9

## RESULT 7

NO40\_LOTJA STANDARD; PRT; 12 AA.  
 AC 022426;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE EARLY NODULIN 40.

GN ENOD40.  
 OS Lotus japonicus.  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
 OC Fabales; Fabaceae; Papilionoideae; Lotus.  
 NC NCBI\_TaxID=34305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. GIFU.  
 RA Chian R.-J., Gresshoff P.M.;  
 RT "Isolation and primary characterization of genomic Enod40 gene from Lotus japonicus cultivar 'Gifu'.";  
 RL (in) Plant Gene Register PG97-142.  
 CC -1- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY SIMILARITY).  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE DEVELOPMENT.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL; AF013594; AAB82785.1; -;  
 KW Nodulation.  
 SQ SEQUENCE 12 AA; 1480 MW; 3C61E8257CB326C3 CRC64;

Query Match 13.68; Score 3; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 WOK 19  
 Db 5 WOK 7

## RESULT 8

NO40\_SESRO STANDARD; PRT; 12 AA.  
 AC 024369;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE EARLY NODULIN 40.  
 GN ENOD40.  
 OS Sesbania rostrata.  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
 OC Fabales; Fabaceae; Papilionoideae; Sesbania.  
 NC NCBI\_TaxID=3895;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Stem nodules;  
 RX MEDLINE=98281575; PubMed=9620265;  
 RA Corich V., Goormachtig S., Lievens S., van Montagu M., Holsters M.;  
 RT "Patterns of ENOD40 gene expression in stem-borne nodules of Sesbania rostrata.";  
 RL Plant Mol. Biol. 37:67-76(1998).  
 CC -1- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY SIMILARITY).  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE DEVELOPMENT.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CR EMBL: Y12714; CAA73252.1; -.  
 KM Modulation.  
 SQ SEQUENCE 12 AA; 1418 MW; 3C6955187CB326C3 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 WQK 19  
 |||  
 Db 5 WQK 7

RESULT 9  
 ID TM2A\_METMA STANDARD; PRT; 12 AA.  
 AC P80652;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE ALTERNATIVE TETRAHYDROMETHANOPTERIN S-METHYLTRANSFERASE 28 KDA SUBUNIT  
 DE (RC 2.1.1.86) (N5-METHYL-TETRAHYDROMETHANOPTERIN--COENZYME M  
 DE METHYLTRANSFERASE 28 KDA SUBUNIT) (FRAGMENT).  
 OS Methanosarcina mazei.  
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;  
 OC Methanosarcina.  
 OX NCBI\_TaxID=2209;  
 RN [1]  
 RP SEQUENCE.

RC STRAIN=DSM 3647 / GOEL.  
 RX MEDLINE=96370840; PubMed=8774736;  
 RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;  
 RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:  
 RT coenzyme M methyltransferase from Methanosarcina mazei Gol  
 RT reconstituted in ether lipid liposomes.";  
 RL Eur. J. Biochem. 239:857-864(1996).

CC -1- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN  
 CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND  
 CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-  
 CC TETRAHYDROMETHANOPTERIN.

CC -1- CATALYTIC ACTIVITY: 5-METHYL-5,6,7,8-TETRAHYDROMETHANOPTERIN +  
 CC 2-MERCAPTOETHANESULFONATE = 5,6,7,8-TETRAHYDROMETHANOPTERIN +  
 CC 2-(METHYLTHIO)ETHANESULFONATE.

CC -1- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

KM Transferase; Methyltransferase; Transmembrane; Methanogenesis.  
 FT NON\_TER 12  
 FT SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 13.6%; Score 3; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 KLE 21  
 |||  
 Db 3 KLE 5

RESULT 10  
 ID IDHA\_CANFA STANDARD; PRT; 13 AA.  
 AC P54836;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT ALPHA, MITOCHONDRIAL  
 DE (RC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH)

DE (FRAGMENT).  
 GN IDH3A.  
 OS Canis familiaris (Dog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).

CC -1- CATALYTIC ACTIVITY: ISOCITRATE + NAD(+) = 2-OXOGULONATE +  
 CC CO(2) + NADH.

CC -1- SUBUNIT: HETEROOLIGOMER OF SUBUNITS ALPHA, BETA, AND GAMMA IN THE  
 CC APPARENT RATIO OF 2:1:1 (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.

CC DEHYDROGENASES FAMILY.  
 CC HSC-2DPAGE: P54836; DOG.

DR InterPro: IPR001804; -.

DR PROSITE: PS00470; IDH\_1MDB; PARTIAL.

KM Oxidoreductase; NAD; Tricarboxylic acid cycle; Mitochondrion.  
 FT NON\_TER 13  
 FT SEQUENCE 13 AA; 1356 MW; 9ABFBC2BA34B2D1 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VQT 15  
 |||  
 Db 4 VQT 6

RESULT 11  
 ID NO40\_PEA STANDARD; PRT; 13 AA.  
 AC P55959;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE EARLY NODULIN 40.  
 GN ENOD40.

OS Pisum sativum (Garden pea).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

OC Fabales; Fabaceae; Papilionoideae; Pisum.

OX NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=CV. SPARKLE; TISSUE=Root nodules;

RX MEDLINE=95036021; PubMed=794896;

RA Matvienko M., van de Sande K., Yang W.C., van Kammen A., Bisseling T.,  
 RA Franssen H.J.;

RT "Comparison of soybean and pea ENOD40 cDNA clones representing genes  
 RT expressed during both early and late stages of nodule development.";  
 RL Plant Mol. Biol. 26:487-493(1994).

CC -1- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT  
 CC GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY  
 CC SIMILARITY).

CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE  
 CC DEVELOPMENT.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>



CC or send an email to [license@lsb-sib.ch](mailto:license@lsb-sib.ch).

CC EMBL: X81064; NOT\_ANNOTATED\_CDS.

KW Nucleotide. 13 AA; 1565 MW; 3C695B66BD8A26C3 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.4e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 WOK 19

Db 6 WOK 8

RESULT 12

NO40\_VICSA STANDARD; PRT; 13 AA.

AC P55961;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE EARLY MODULIN 40.

ENOD40.

OS Eukaryota (Spring vetch) (Tare).

OC Magnoliophyta; eudicotyledons; core eudicots; rosids I;

OC Fabales; Fabaceae; Papilionoideae; Vicia.

OX NCBI\_TaxID=3908;

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIGRA; TISSUE=Root nodules;

RX MEDLINE=96011756; PubMed=7548828;

RA Vijn I., Tang W.-C., Pallinggaard N., Oestergaard Jensen E.,

van Kamen A., Bisseling T.;

\*VSEND05, VSEND012 and VSEND040 expression during Rhizobium-induced

RT nodule formation on *Vicia sativa* roots.;

RT Plant Mol. Biol. 28:1111-1119(1995).

- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT

GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY

SIMILARITY).

- DEVELOPMENTAL STAGE: EXPRESSED DURING RHIZOBIUM-INDUCED NODULE

FORMATION. IN 4-DAY OLD NODULES IT IS FOUND IN ALL THE CELLS OF

THE CENTRE OF THE NODULE PRIMORDIUM AND ALSO OCCURS IN THE REGION

OF THE ROOT PERICICLE FACING THE NODULE PRIMORDIUM. AT DAY 5,

EXPRESSION IS SEEN IN THE COMPLETE CENTRAL TISSUE. AT DAY 20

EXPRESSED IN THE COMPLETE PREFIXATION ZONE II, AND IN THE PROXIMAL

PART OF THIS ZONE IT IS FOUND ONLY IN THE INFECTED CELLS BUT NOT

IN THE UNINFECTED CELLS. AT THE TRANSITION OF PREFIXATION ZONE II

INTO INTERZONE II-III EXPRESSION DECREASES IN THE UNINFECTED CELLS.

OY 17 WOK 19

Db 6 WOK 8

RESULT 13

UVRD\_SALTY

ID UVRD\_SALTY

AC 005311;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DE DNA HELICASE II (EC 3.6.1.-) (FRAGMENT).

GN UVRD.

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.

OX NCBI\_TaxID=602;

RP SEQUENCE FROM N.A.

RX MEDLINE=93300725; PubMed=8314774;

RA Smith R.L., Banks J.L., Snively M.D., Maguire M.E.;

"Sequence and topology of the *CorA* magnesium transport systems of

*Salmonella typhimurium* and *Escherichia coli*. Identification of a new

RT class of transport protein.;"

RT J. Biol. Chem. 268:14071-14080(1993).

- FUNCTION: HAS BOTH ATPASE AND HELICASE ACTIVITIES. UNWINDS DNA

DOUBLES WITH 3' TO 5' POLARITY WITH RESPECT TO THE BOUND STRAND

AND INITIATES UNWINDING MOST EFFECTIVELY WHEN A SINGLE-STRANDED

REGION IS PRESENT. INVOLVED IN THE POSTINCISION EVENTS OF

NUCLEOTIDE EXCISION REPAIR AND METHYL-DIRECTED MISMATCH REPAIR.

- SIMILARITY: BELONGS TO THE UVRD SUBFAMILY OF HELICASES.

-----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.lsb-sib.ch/announce/>

CC or send an email to [license@lsb-sib.ch](mailto:license@lsb-sib.ch)).

CC EMBL: L11043; AAA02965.1; -

DR SLYGene: SGI0414; uvrD.

KW DNA-binding.

KW SOS response; Helicase; ATP-binding;

FT NON\_TER

SEQUENCE 13 AA; 1492 MW; D7967B28B09ACB5D CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 KLE 21

Db 9 KLE 11

RESULT 14

COX1\_THROB

ID COX1\_THROB

AC P80979;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIA (EC 1.9.3.1) (FRAGMENT).

OS Thunnus obesus (Bigeye tuna).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;

OX NCBI\_TaxID=8241;

[1]

RP SEQUENCE.  
RC TISSUE-Heart, and Liver;  
RX MEDLINE=97454291; PubMed=9310366;  
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,  
RA Kadenbach B.;  
RT "The subunit structure of cytochrome-c oxidase from tuna heart and  
RT liver.";  
RL Eur. J. Biochem. 248:99-103(1997).  
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
CC MITOCHONDRIAL ELECTRON TRANSPORT.  
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +  
CC 4 FERRICYTOCHROME C.  
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.  
KM Oxidoreductase; Inner membrane; Mitochondrion.  
FT MOD\_RES 1 1 BLOCKED.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1769 MW; C11B99419E69A1E CRC64;

Query Match 13.6%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 OKL 20  
|||  
Db 8 OKL 10

RESULT 15  
PDGB\_PIG STANDARD; PRT; 15 AA.  
AC P20034:  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE PLATELET-DERIVED GROWTH FACTOR, B CHAIN (PDGF B-CHAIN) (PDGFB)  
DE (FRAGMENT).  
GN PDGFB.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=85126898; PubMed=6526008;  
RA Stroobant P., Waterfield M.D.;  
RT "Purification and properties of porcine platelet-derived growth  
RT factor.";  
RL EMBO J. 3:2963-2967(1984).  
CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR  
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS  
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS  
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE  
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.  
CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A  
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN  
CC TRANSFORMATION PROCESSES.  
CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE  
CC PDGF RECEPTOR.  
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
CC PIR: A22789; A22789.  
DR InterPro: IPR000072; -  
DR PROSITE: PS00249; PDGF\_1; PARTIAL.  
DR PROSITE: PS50278; PDGF\_2; PARTIAL.  
KM Mitogen; Growth factor; Proto-oncogene; Platelet.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1411 MW; DCC39014450251C2 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 11 PAV 13  
|||  
Db 5 PAV 7

Search completed: July 23, 2001, 17:04:49  
Job time: 510 sec



**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:52:58 ; Search time 41.27 Seconds  
(without alignments)  
40.607 Million cell updates/sec

Title: US-09-351-296-12

Perfect score: 22

Sequence: 1 TASRHAETVTPAVQTNMOKLEV 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4035

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

1: PIR.68:\*  
2: pir1:\*  
3: pir2:\*  
4: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	18.2	6	2	S02617
2	3	13.6	6	2	B31263
3	3	13.6	6	2	PT0518
4	3	13.6	6	2	PT0662
5	3	13.6	7	2	JN0859
6	3	13.6	7	2	P00727
7	3	13.6	7	2	PT0671
8	3	13.6	8	1	LFSAME
9	3	13.6	8	2	PT0726
10	3	13.6	9	2	A31576
11	3	13.6	9	2	PT0326
12	3	13.6	9	2	B46250
13	3	13.6	9	2	PC7074
14	3	13.6	10	2	B33710
15	3	13.6	10	2	A39745
16	3	13.6	10	2	P00783
17	3	13.6	10	2	PS0209
18	3	13.6	10	2	S43631
19	3	13.6	10	2	PH1592
20	3	13.6	10	2	PH0936
21	3	13.6	11	2	S21727
22	3	13.6	11	2	PT0217
23	3	13.6	11	2	PH0929
24	3	13.6	11	2	PH0947
25	3	13.6	11	2	PH0919
26	3	13.6	11	2	I52304
27	3	13.6	12	2	A28856
28	3	13.6	12	2	S43013
29	3	13.6	12	2	JU0356

30	3	13.6	12	2	A33099	163k exoantigen -
31	3	13.6	12	2	PT0257	Ig heavy chain CRD
32	3	13.6	12	2	S74196	3-hydroxy-3-methyl
33	3	13.6	12	2	C20907	Ig kappa-1 chain J
34	3	13.6	12	2	F20907	Ig kappa-2 chain J
35	3	13.6	13	2	D61491	seed protein ws-4
36	3	13.6	13	2	S60046	early nodulin 40 -
37	3	13.6	13	2	A40207	cell surface glyco
38	3	13.6	13	2	PC1149	equinotoxin 1A - s
39	3	13.6	13	2	B61233	conceptus protein
40	3	13.6	13	2	C53275	Ig kappa-1 chain J
41	3	13.6	13	2	E53275	Ig kappa-1 chain J
42	3	13.6	13	2	I49637	deoxy nucleotidyltr
43	3	13.6	13	2	H33932	Ig kappa chain J r
44	3	13.6	13	2	A33932	Ig kappa chain J r
45	3	13.6	13	2	A32486	beta protein - rat

#### ALIGNMENTS

RESULT 1  
S02617  
alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)  
C:Species: Equus caballus (domestic horse)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 31-Jan-1997  
C:Accession: S02617  
R:Fairwell, T.; Julia, P.; Kaiser, R.; Holmquist, B.; Pares, X.; Vallee, B.L.; Joernv  
FEBS Lett. 222, 99-103, 1987  
A:Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differ  
A:Reference number: S02617; MUID:88005160  
A:Accession: S02617  
A:Molecule type: protein  
A:Residues: 1-6 <FAI>  
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 18.2%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEVI 9  
DB 2 AEVI 5

RESULT 2  
B31263  
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodiu  
C:Species: Plasmodium falciparum  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Mar-1996  
C:Accession: B31263  
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.  
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988  
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate syntha  
A:Reference number: A94217; MUID:89057886  
A:Accession: B31263  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-6 <PET>  
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 13.6%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 TNW 17  
DB 1 TNW 3

```
RESULT 3
PT0518
T-cell receptor beta chain V-D-J region (100-4B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0518
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0518
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 13.6%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASR 4
   |||
Db 1 ASR 3

RESULT 4
PT0662
T-cell receptor beta chain V-D-J region (121-3BA) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0662
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0662
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FE>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 13.6%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASR 4
   |||
Db 1 ASR 3

RESULT 5
JN0859
peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito
C:Species: Sarda orientalis (striped bonito)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: JN0859
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe
A:Reference number: JN0859; MUID:94080036
A:Accession: JN0859
A:Molecule type: protein
A:Residues: 1-7 <MAT>
A:Experimental source: intestine
C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensi
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor
```

```
Query Match 13.6%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 KLE 21
   |||
Db 4 KLE 6

RESULT 6
PQ0727
H2 class I protein [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PQ0727
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library: a data-file of rice proteins separated by two-dimens
A:Reference number: PQ0696
A:Accession: PQ0727
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <KOM>

Query Match 13.6%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PAV 13
   |||
Db 3 PAV 5

RESULT 7
PT0671
T-cell receptor beta chain V-D-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 04-Mar-2000
C:Accession: PT0671; PT0564; PT0537; PT0536; PT0682
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0671
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-7 <FE>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 140-1K
A:Accession: PT0564
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FE1>
A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1CE
A:Accession: PT0537
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FE2>
A:Experimental source: adult thymus, strain BALB/c, clone 126-1CH
A:Accession: PT0536
A:Status: translation not shown
A:Molecule type: protein
A:Residues: 1-3 <FE3>
A:Experimental source: adult thymus, strain BALB/c, clone 126-1CC
A:Accession: PT0682
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-3 <FE4>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 140-1B
C:Keywords: T-cell receptor
```

Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASR 4  
|||  
Db 1 ASR 3

## RESULT 8

LFSAME

probable msra leader peptide - Staphylococcus epidermidis

C:Species: Staphylococcus epidermidis

C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

C:Accession: S1157

R:Ross, J.I.; Eady, E.A.; Cove, J.H.; Cunliffe, W.J.; Baumberg, S.; Wootton, J.C.

Mol. Microbiol. 4, 1207-1214, 1990

A:Title: Inducible erythromycin resistance in staphylococci is encoded by a member of th

A:Reference number: S1157; MUID:91041730

A:Accession: S1157

A:Molecule type: DNA

A:Residues: 1-8 &lt;ROS&gt;

A:Cross references: EMBL:X52085; NID:947000; PIDN:CA36303.1; PID:9581653

C:Superfamily: probable msra leader peptide

Query Match 13.6%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAS 3  
|||  
Db 2 TAS 4

## RESULT 9

unidentified 4.5/45k [imported] - rice (fragment)

C:Species: Oryza sativa (rice)

C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C:Accession: PQ0726

R:Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A:Title: A rice protein library: a data-file of rice proteins separated by two-dimension

A:Reference number: PQ0696

A:Accession: PQ0726

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 &lt;KOM&gt;

Query Match 13.6%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AVQ 14  
|||  
Db 1 AVQ 3

## RESULT 10

xylose isomerase (EC 5.3.1.5), intracellular - Streptomyces sp. (fragment)

C:Species: Streptomyces sp.

C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 28-Apr-1993

C:Accession: A31576

R:Patwar, H.S.; Kannan, K.; Srinivasan, M.C.; Vartak, H.G.

Biochem. Biophys. Res. Commun. 155, 411-417, 1988

A:Title: Purification and characterisation of glucose (xylose) isomerase from Chainia sp

A:Reference number: A31576; MUID:88326335

A:Accession: A31576

A:Contents: Chainia sp. NCL 82-5-1

A:Molecule type: protein

A:Residues: 1-9 &lt;PAW&gt;

C:Keywords: Intramolecular oxidoreductase; isomerase

Query Match 13.6%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RHA 6  
|||  
Db 1 RHA 3

## RESULT 11

PT0326

Ig heavy chain CRD3 region (clone J2-109) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PT0326

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0326

A:Molecule type: DNA

A:Residues: 1-9 &lt;YAM&gt;

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 13.6%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PAV 13  
|||  
Db 3 PAV 5

## RESULT 12

B46250

alpha-adaptin - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 05-Apr-1995

C:Accession: B46250

R:Timmerman, A.P.; Mayrlethner, M.M.; Lukas, T.J.; Chadwick, C.C.; Saito, A.; Walterso

Proc. Natl. Acad. Sci. U.S.A. 89, 8976-8980, 1992

A:Title: Inositol polyphosphate receptor and clathrin assembly protein AP-2 are relat

A:Reference number: A46250; MUID:93028388

A:Accession: B46250

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 &lt;TIM&gt;

Query Match 13.6%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PAV 13  
|||  
Db 1 PAV 3

## RESULT 13

PC7074

translation elongation factor eEF-1 beta chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000

C:Accession: PC7074

R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y

Electrophoresis 21, 1853-1871, 2000

A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles o

A:Reference number: PC7072

A:Accession: PC7074  
A:Molecule type: protein  
A:Residues: 1-9 <TSU>  
A:Experimental source: strain C57BL/6Cr SLC, male; brain, cortex  
C:Keywords: brain, cerebral cortex

Query Match 13.6%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

OY 10 TPA 12  
|||  
Db 7 TPA 9

RESULT 14  
B33710  
ornithine decarboxylase leader peptide - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 24-Sep-1999  
C:Accession: B33710  
R:Wen, L.; Huang, J.K.; Blackshear, P.J.  
J. Biol. Chem. 264, 9016-9021, 1989  
A:Title: Rat ornithine decarboxylase gene. Nucleotide sequence, potential regulatory ele  
A:Reference number: A33710; MUID:89255378  
A:Accession: B33710  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-10 <WEN>  
A:Cross-references: GB:J04791; NID:9205807; PIDN:AAA66163.1; PID:9806309  
C:Superfamily: unassigned leader peptides

Query Match 13.6%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

OY 2 ASR 4  
|||  
Db 4 ASR 6

RESULT 15  
A39745  
endo-glucosylceramidase activator II - Rhodococcus sp. (fragment)  
C:Species: Rhodococcus sp.  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993  
C:Accession: A39745  
R:Ito, M.; Ikegami, Y.; Yamagata, T.  
J. Biol. Chem. 266, 7919-7926, 1991  
A:Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosceramidases. E  
ble using these activator proteins.  
A:Reference number: A39745; MUID:91210321  
A:Accession: A39745  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <ITO>

Query Match 13.6%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

OY 9 ITP 11  
|||  
Db 4 ITP 6

Search completed: July 23, 2001, 16:57:40  
Job time: 282 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:52:23 ; Search time 34.6 Seconds  
(without alignments)  
12.809 Million cell updates/sec

Title: US-09-351-296-12

Perfect score: 22

Sequence: 1 TASSRAHEVITPAVQTNMOKLEV 22

Scoring table: OLIGO

Searched: 193259 seqs, 20144635 residues

Word size: 0

Total number of hits satisfying chosen parameters: 93443

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database: Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PCBUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	US-08-845-926-12	Sequence 12, Appl
2	11	50.0	22	US-08-845-926-11	Sequence 11, Appl
3	10	45.5	19	US-08-604-365-11	Sequence 11, Appl
4	5	22.7	15	US-08-447-411-64	Sequence 64, Appl
5	5	22.7	15	US-08-662-227-21	Sequence 21, Appl
6	5	22.7	15	US-08-662-227-22	Sequence 22, Appl
7	5	22.7	17	US-08-300-928C-54	Sequence 54, Appl
8	5	22.7	17	US-08-430-944D-54	Sequence 54, Appl
9	5	22.7	17	US-08-430-014-54	Sequence 54, Appl
10	5	22.7	17	US-08-431-184-54	Sequence 54, Appl
11	5	22.7	18	US-09-100-789-5	Sequence 5, Appl1
12	4	18.2	6	US-08-478-386A-36	Sequence 36, Appl
13	4	18.2	6	US-08-292-597-36	Sequence 36, Appl
14	4	18.2	6	US-08-388-653-36	Sequence 36, Appl
15	4	18.2	6	US-08-473-985-36	Sequence 36, Appl
16	4	18.2	6	US-08-483-898-36	Sequence 36, Appl
17	4	18.2	6	US-09-087-716-36	Sequence 36, Appl
18	4	18.2	6	US-09-157-753-36	Sequence 36, Appl
19	4	18.2	6	US-09-157-330-36	Sequence 36, Appl
20	4	18.2	6	US-09-087-811-36	Sequence 36, Appl
21	4	18.2	6	US-09-156-855-36	Sequence 36, Appl
22	4	18.2	6	US-09-158-010-36	Sequence 36, Appl
23	4	18.2	6	US-09-087-647-36	Sequence 36, Appl
24	4	18.2	7	US-08-666-473-58	Sequence 36, Appl
25	4	18.2	7	US-08-340-283-88	Sequence 88, Appl
26	4	18.2	8	US-07-670-296-4	Sequence 4, Appl1
27	4	18.2	8	US-08-093-781-5	Sequence 5, Appl1

28	4	18.2	9	US-07-670-296-3	Sequence 3, Appl1
29	4	18.2	9	US-08-093-781-4	Sequence 4, Appl1
30	4	18.2	9	US-07-721-761A-9	Sequence 9, Appl1
31	4	18.2	9	US-07-978-687-9	Sequence 9, Appl1
32	4	18.2	9	US-08-340-283-95	Sequence 95, Appl
33	4	18.2	9	US-08-146-028-343	Sequence 343, App
34	4	18.2	9	US-08-146-028-344	Sequence 344, App
35	4	18.2	9	US-08-146-028-345	Sequence 345, App
36	4	18.2	9	US-08-146-028-349	Sequence 349, App
37	4	18.2	9	US-08-146-028-350	Sequence 350, App
38	4	18.2	9	US-08-146-028-351	Sequence 351, App
39	4	18.2	9	US-08-146-028-352	Sequence 352, App
40	4	18.2	9	US-08-146-028-353	Sequence 353, App
41	4	18.2	9	US-08-146-028-355	Sequence 355, App
42	4	18.2	9	US-08-146-028-355	Sequence 355, App
43	4	18.2	9	US-08-146-028-356	Sequence 356, App
44	4	18.2	9	US-08-146-028-357	Sequence 357, App
45	4	18.2	9	US-08-146-028-358	Sequence 358, App

#### ALIGNMENTS

RESULT 1  
US-08-845-926-12  
Sequence 12, Application US/08845926  
Patent No. 5935778  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike  
APPLICANT: SCHMITT, Urban  
APPLICANT: JUNG, G. nther-Gerhard  
APPLICANT: IHLENFELDT, HANS-Georg  
TITLE OF INVENTION: Method for serological typing using  
TITLE OF INVENTION: type-specific antigens  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845,926  
FILING DATE: 04-28-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/598,993  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 04 302.2  
FILING DATE: 09-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:

ORGANISM: Hepatitis C Virus  
US-08-845-926-12

Query Match 100.0%; Score 22; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1,3e-17;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TASRAHEVITPAVOTNMOKLE 22  
1 TASRAHEVITPAVOTNMOKLE 22

RESULT 2  
US-08-845-926-11  
Sequence 11, Application US/08845926  
Patent No. 5935778

GENERAL INFORMATION:

APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike

APPLICANT: SCHMITT, Urban

APPLICANT: JUNG, G nther-Gerhard

APPLICANT: IHLENFELDT, HANS-Georg

APPLICANT: KRAAS, Wolfgang

TITLE OF INVENTION: Method for serological typing using

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESSES:

STREET: 655 Fifteenth Street N.W. Suite 330

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/845,926

FILING DATE: 04-28-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/598,993

FILING DATE: 09-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 195 04 302.2

FILING DATE: 09-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Murray, Robert B.

REGISTRATION NUMBER: 22,980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)638-5000

TELEFAX: (202)638-4810

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Hepatitis C Virus

US-08-845-926-11

Query Match 50.0%; Score 11; DB 2; Length 22;

Best Local Similarity 100.0%; Pred. No. 9e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PAVOTNMOKLE 21  
11 PAVOTNMOKLE 21

Db 11 PAVOTNMOKLE 21

RESULT 3

US-08-604-365-11

Sequence 11, Application US/08604365

Patent No. 6183949

GENERAL INFORMATION:

APPLICANT: Seidel, Christoph; Ehrlich-Weinreich,

APPLICANT: Gertraud; Bayer, Hubert; Wiennues, Ursula; Jung,

APPLICANT: G nther-Gerhard; Ihlenfeldt, Hans Georg

TITLE OF INVENTION: HCV Peptide Antigens and Methods for

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/604,365

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/977,398

FILING DATE: 11-MARCH-1993

APPLICATION NUMBER: PCT/EP92/01468

FILING DATE: 30-JUNE-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 41 22 160.5

FILING DATE: 04-JULY-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 41 41 304.0

FILING DATE: 14-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 42 09 216.9

FILING DATE: 21-MARCH-1992

ATTORNEY/AGENT INFORMATION:

NAME: Tsai, Christine H.

REGISTRATION NUMBER: 34,266

REFERENCE/DOCKET NUMBER: BOER 1010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-604-365-11

Query Match 45.5%; Score 10; DB 4; Length 19;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 AVOTNMOKLE 21  
1 AVOTNMOKLE 10

RESULT 4

US-08-447-411-64

Sequence 64, Application US/08447411

Patent No. 5773243

GENERAL INFORMATION:  
APPLICANT: FRITZINGER, DAVID C.  
APPLICANT: BREDEHORST, REINHARD  
APPLICANT: VOGEL, CARL-WILHELM  
TITLE OF INVENTION: DNA ENCODING COBRA C3, CWF1, AND CWF2  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P. C. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/447,411  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/043,747  
FILING DATE: 07-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, No. 3773243man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-101-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Naja naja  
US-08-447-411-64

Query Match 22.7%; Score 5; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 ITPAV 13  
Db 6 ITPAV 10

RESULT 5  
US-08-662-227-21  
Sequence 21, Application US/08662227  
Patent No. 3922320  
GENERAL INFORMATION:  
APPLICANT: VOGEL, CARL-WILHELM  
APPLICANT: BREDEHORST, REINHORST  
APPLICANT: KOCK, MICHAEL  
APPLICANT: FRITZINGER, DAVID  
TITLE OF INVENTION: RECOMBINANT PROCV  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P. C. Jefferson Davis Highway  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/662,227  
FILING DATE: 14-JUN-1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-0107-0X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-662-227-21

Query Match 22.7%; Score 5; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 ITPAV 13  
Db 6 ITPAV 10

RESULT 6  
US-08-662-227-22  
Sequence 22, Application US/08662227  
Patent No. 3922320  
GENERAL INFORMATION:  
APPLICANT: VOGEL, CARL-WILHELM  
APPLICANT: BREDEHORST, REINHORST  
APPLICANT: KOCK, MICHAEL  
APPLICANT: FRITZINGER, DAVID  
TITLE OF INVENTION: RECOMBINANT PROCV  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P. C. Jefferson Davis Highway  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/662,227  
FILING DATE: 14-JUN-1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-0107-0X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-662-227-22

Query Match 22.7%; Score 5; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 ITPAV 13  
|||||  
Db 6 ITPAV 10

RESULT 7  
US-08-300-928C-54  
Sequence 54, Application US/08300928C  
Patent No. 6019972  
GENERAL INFORMATION:  
APPLICANT: GEFTER, MALCOLM L. et al.  
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02145  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/300,928C  
FILING DATE: September 2, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/807,529  
FILING DATE: December 13, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: AMY E. MANDRAGOURAS  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: 002.GUS(IMI-044)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-300-928C-54

Query Match 22.7%; Score 5; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 ITPAV 13  
|||||  
Db 2 ITPAV 6

RESULT 8  
US-08-430-944D-54

Sequence 54, Application US/08430944D  
Patent No. 6025162  
GENERAL INFORMATION:  
APPLICANT: Bruce L. Rogers et al.  
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,944D  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/430,014  
FILING DATE: 27-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,928  
FILING DATE: 02-SEPT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-044DV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-430-944D-54

Query Match 22.7%; Score 5; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 ITPAV 13  
|||||  
Db 2 ITPAV 6

RESULT 9  
US-08-430-014-54  
Sequence 54, Application US/08430014  
Patent No. 6048962  
GENERAL INFORMATION:  
APPLICANT: GEFTER, MALCOLM L. et al.  
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02145  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,014  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/300,928  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: AMY E. MANDRAGOURAS  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: 002.6US(IMT-044)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-430-014-54

Query Match 22.7%; Score 5; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 ITPAV 13  
Db 2 ITPAV 6

RESULT 10  
US-08-431-184-54  
Sequence 54, Application US/08431184  
Patent No. 6120769  
GENERAL INFORMATION:  
APPLICANT: Bruce L. Rogers et al.  
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/431,184  
FILING DATE: 28-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/430,014  
FILING DATE: 27-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,928  
FILING DATE: 02-SEPT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-044DV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
COMPUTER READABLE FORM:

INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-431-184-54

Query Match 22.7%; Score 5; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 ITPAV 13  
Db 2 ITPAV 6

RESULT 11  
US-09-100-789-5  
Sequence 5, Application US/09100789A  
Patent No. 6011013  
GENERAL INFORMATION:  
APPLICANT: Carr et al.  
TITLE OF INVENTION: No. 6011013el Contraceptive Compositions and Methods  
FILE REFERENCE: 50379  
CURRENT APPLICATION NUMBER: US/09/100,789A  
CURRENT FILING DATE: 1998-06-18  
EARLIER APPLICATION NUMBER: 60/050,314  
EARLIER FILING DATE: 1997-06-20  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-100-789-5

Query Match 22.7%; Score 5; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AEVIT 10  
Db 8 AEVIT 12

RESULT 12  
US-08-478-386A-36  
Sequence 36, Application US/08478386A  
Patent No. 5830462  
GENERAL INFORMATION:  
APPLICANT: Crabtree, Gerald R.  
APPLICANT: Schreiber, Stuart L.  
APPLICANT: Spencer, David M.  
APPLICANT: Wandless, Thomas J.  
APPLICANT: Belshaw, Peter  
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
STREET: 26 Landsdowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC/DOS/MS/DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478.386A  
FILING DATE: 07/JUN/1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Figg, E. Anthony  
REGISTRATION NUMBER: 27,195  
REFERENCE/DOCKET NUMBER: 2054-114A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-478-386A-36

Query Match 18.2%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 KLEV 22  
1111  
Db 3 KLEV 6

RESULT 13  
US-08-292-597-36  
Sequence 36, Application US/08292597  
Patent No. 5834266  
GENERAL INFORMATION:  
APPLICANT: Gerald R. Crabtree  
APPLICANT: Schreiber, Stuart L.  
APPLICANT: Spencer, David M.  
APPLICANT: Wandless, Thomas J.  
APPLICANT: Belshaw, Peter  
TITLE OF INVENTION: Regulated Apoptosis  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
STREET: 26 Landsdowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC/DOS/MS/DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292.597  
FILING DATE: 18/AUG/1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Figg, E. Anthony  
REGISTRATION NUMBER: 27,195  
REFERENCE/DOCKET NUMBER: 2054-108A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-292-597-36

Query Match 18.2%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 KLEV 22  
1111  
Db 3 KLEV 6

RESULT 14  
US-08-388-653-36  
Sequence 36, Application US/08388653  
Patent No. 5869337  
GENERAL INFORMATION:  
APPLICANT: Crabtree, Gerald R.  
APPLICANT: Schreiber, Stuart L.  
APPLICANT: Spencer, David M.  
APPLICANT: Wandless, Thomas J.  
APPLICANT: Belshaw, Peter  
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED  
GENES AND OTHER BIOLOGICAL EVENTS  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
STREET: 26 Landsdowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC/DOS/MS/DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388.653  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478.386  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Figg, E. Anthony  
REGISTRATION NUMBER: 27,195  
REFERENCE/DOCKET NUMBER: 2054-114A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-388-653-36

Query Match 18.2%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 KLEV 22  
1111  
Db 3 KLEV 6

RESULT 15  
US-08-473-985-36  
; Sequence 36, Application US/08473985  
; Patent No. 5871753  
; GENERAL INFORMATION:  
; APPLICANT: Crabtree, Gerald R.  
; APPLICANT: Schreider, Stuart L.  
; APPLICANT: Spencer, David M.  
; APPLICANT: Wandless, Thomas J.  
; APPLICANT: Belshaw, Peter  
; APPLICANT: Ho, Steffan  
; TITLE OF INVENTION: Regulated Transcription of Targeted Genes and  
; TITLE OF INVENTION: Other Biological Events  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/473,985  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/179,748  
; FILING DATE: 07-JAN-1994  
; ATTORNEY/AGENT INFORMATION: .  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-SU 9863  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-473-985-36

Query Match 18.2%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 KLEV 22  
|||  
Db 3 KLEV 6

Search completed: July 23, 2001, 16:56:52  
Job time: 269 sec

This Page Blank (uspto)



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 16:47:23 ; Search time 65.41 Seconds  
(without alignments)  
20.390 Million cell updates/sec

Title: US-09-351-296-12

Perfect score: 22

Sequence: 1 TASRHAETITPAVQTNMQKLEY 22

Scoring table: OLIGO

Searched: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 148088

Minimum DB seq length: 6

Maximum DB seq length: 22

Post-processing: Listing first 45 summaries

Database :

A\_Geneseq\_0601:\*

1: /SIDS8/gcgdata/geneseq/AA1980.DAT:\*  
2: /SIDS8/gcgdata/geneseq/AA1981.DAT:\*  
3: /SIDS8/gcgdata/geneseq/AA1982.DAT:\*  
4: /SIDS8/gcgdata/geneseq/AA1983.DAT:\*  
5: /SIDS8/gcgdata/geneseq/AA1984.DAT:\*  
6: /SIDS8/gcgdata/geneseq/AA1985.DAT:\*  
7: /SIDS8/gcgdata/geneseq/AA1986.DAT:\*  
8: /SIDS8/gcgdata/geneseq/AA1987.DAT:\*  
9: /SIDS8/gcgdata/geneseq/AA1988.DAT:\*  
10: /SIDS8/gcgdata/geneseq/AA1989.DAT:\*  
11: /SIDS8/gcgdata/geneseq/AA1990.DAT:\*  
12: /SIDS8/gcgdata/geneseq/AA1991.DAT:\*  
13: /SIDS8/gcgdata/geneseq/AA1992.DAT:\*  
14: /SIDS8/gcgdata/geneseq/AA1993.DAT:\*  
15: /SIDS8/gcgdata/geneseq/AA1994.DAT:\*  
16: /SIDS8/gcgdata/geneseq/AA1995.DAT:\*  
17: /SIDS8/gcgdata/geneseq/AA1996.DAT:\*  
18: /SIDS8/gcgdata/geneseq/AA1997.DAT:\*  
19: /SIDS8/gcgdata/geneseq/AA1998.DAT:\*  
20: /SIDS8/gcgdata/geneseq/AA1999.DAT:\*  
21: /SIDS8/gcgdata/geneseq/AA2000.DAT:\*  
22: /SIDS8/gcgdata/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	17	AA99902
2	11	50.0	22	17	AA99901
3	10	45.5	19	14	AA30982
4	5	22.7	17	21	AA328959
5	5	22.7	17	21	AA87702
6	5	22.7	17	21	AA90114
7	5	22.7	17	21	AA51499
8	5	22.7	18	19	AA61105
9	5	22.7	18	21	AA56950
10	4	18.2	6	17	AAW05816
11	4	18.2	6	19	AAW6749

12	4	18.2	6	20	AAW92484	Murine signalling
13	4	18.2	6	21	AA803568	Murine signalling
14	4	18.2	6	21	AA90488	Peptide encoded by
15	4	18.2	6	22	AA860832	Peptide #14 encode
16	4	18.2	6	22	AA836957	Peptide #15 encode
17	4	18.2	7	17	AAW07063	Synthetic peptide
18	4	18.2	7	19	AAW77194	Pharmaceutically a
19	4	18.2	7	20	AAV16884	Heat shock protein
20	4	18.2	7	21	AA809391	Hepatitis GB virus
21	4	18.2	8	18	AAW19825	Universal transfer
22	4	18.2	8	22	AAW70277	Peptide #21. Unid
23	4	18.2	9	16	AA838821	SH3-binding prolin
24	4	18.2	9	17	AAW07070	Synthetic peptide
25	4	18.2	9	20	AAV46863	Immunogenic peptid
26	4	18.2	9	20	AAV17976	Peptide Seq ID No:
27	4	18.2	9	22	AAW5702	HLA class I bindin
28	4	18.2	10	20	AAV46866	Immunogenic peptid
29	4	18.2	10	21	AAV66413	HLA-B40-binding HI
30	4	18.2	11	15	AAW52837	Streptolysin O pep
31	4	18.2	11	16	AAW21333	Glucagon precursor
32	4	18.2	11	19	AAW83280	NPF motif EH domai
33	4	18.2	11	21	AAV69279	Peptide linker use
34	4	18.2	12	15	AAW60701	N-terminal a.a. of
35	4	18.2	12	15	AAW60702	N-terminal a.a. of
36	4	18.2	12	20	AAV36465	Fragment of human
37	4	18.2	12	20	AAW94430	Viral protease-sen
38	4	18.2	12	21	AAV97851	Group A streptococ
39	4	18.2	12	22	AAV72189	Peptide from regio
40	4	18.2	13	21	AAW39624	Anti-IL12 antibody
41	4	18.2	13	21	AAW39669	Anti-IL12 antibody
42	4	18.2	13	21	AAW39677	Anti-IL12 antibody
43	4	18.2	14	14	AAW33104	Human cytomegalovi
44	4	18.2	14	17	AAW97043	Immunogen HPV-18
45	4	18.2	14	21	AAW08246	Peptide derived fr

#### ALIGNMENTS

RESULT	1	
AA99902	standard; peptide: 22 AA.	
ID	AA99902:	
XX	23-APR-1997 (first entry)	
XX	Hepatitis C Virus antigen peptide 12.	
XX	HCV; immunologically reactive; antigen; epitope; screen; typing; antibody; immobilised.	
XX	Hepatitis C Virus.	
XX	EP726463-A2.	
XX	14-AUG-1996.	
XX	09-FEB-1996: 96EP-0101925.	
XX	09-FEB-1995: 95DE-4004302.	
XX	(BOEF ) BOEHRINGER MANNHEIM GMBH.	
XX	Schmitt U, Seidel C, Wlenhues-thelen U;	
XX	WPI; 1996-364504/37.	
XX	Antibody typing by sequential reaction with immobilised antigens - esp. using new hepatitis C virus peptide(s) as antigens	
XX	Claim 9; Page 14; 22pp; German.	

CC AAR9891-920 comprise at least one immunologically active region of  
CC hepatitis C virus (HCV), selected from amino acid sequences 384-414,  
CC 1738-1759, 2217-2236, 2402-2419 and 2345-2357. The peptides are  
CC used in a claimed method for typing antibodies in a 11q. sample.  
CC Assays performed using the peptides as antigens, which corresp. to  
CC regions of high immunogenicity and variability, can be performed  
CC routinely using simple equipment to provide accurate HCV typing.  
CC AAR9901-06 are derived from amino acids 1738-1759 of the NS4-region  
CC of HCV.  
XX  
XX  
SQ Sequence 22 AA;  
  
Query Match 100.0%; Score 22; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.5e-17;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 TASHAEVTPAVQTNQKLEV 22  
Db 1 tasrhaevitpavqtnwqklev 22  
  
RESULT 2  
AAR9901 standard; peptide; 22 AA.  
XX  
AC AAR9901;  
XX  
DT 23-APR-1997 (first entry)  
XX  
DE Hepatitis C Virus antigen peptide 11.  
XX  
KM HCV; immunologically reactive; antigen; epitope; screen; typing;  
KW antibody; immobilised.  
XX  
OS Hepatitis C Virus.  
XX  
PN EP726463-A2.  
XX  
PD 14-AUG-1996.  
XX  
PF 09-FEB-1996; 96EP-0101925.  
XX  
PR 09-FEB-1995; 95DE-4004302.  
XX  
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX  
PI Schmitt U, Seidel C, Wienhues-thelen U;  
XX  
DR WPI; 1996-364504/37.  
XX  
PT Antibody typing by sequential reaction with immobilised antigens -  
PT esp. using new hepatitis C virus peptide(s) as antigens  
XX  
PS Claim 9; Page 13; 22pp; German.  
XX  
CC AAR9891-920 comprise at least one immunologically active region of  
CC hepatitis C virus (HCV), selected from amino acid sequences 384-414,  
CC 1738-1759, 2217-2236, 2402-2419 and 2345-2357. The peptides are  
CC used in a claimed method for typing antibodies in a 11q. sample.  
CC Assays performed using the peptides as antigens, which corresp. to  
CC regions of high immunogenicity and variability, can be performed  
CC routinely using simple equipment to provide accurate HCV typing.  
CC AAR9901-06 are derived from amino acids 1738-1759 of the NS4-region  
CC of HCV.  
XX  
XX  
SQ Sequence 22 AA;

OY 11 PAVQTNQKLE 21  
Db 11 pavqtnwqkle 21  
  
RESULT 3  
AAR30982 standard; peptide; 19 AA.  
XX  
AC AAR30982;  
XX  
DT 11-MAY-1993 (first entry)  
XX  
DE Short HCV antigen sequence (3).  
XX  
KW Hepatitis C virus; antigen; diagnosis; vaccine; C100-3; env; core;  
KW reactive site; binding.  
XX  
OS Hepatitis C virus.  
XX  
PN DE4209215-A.  
XX  
PD 07-JAN-1993.  
XX  
PF 21-MAR-1992; 92DE-4209215.  
XX  
PR 04-JUL-1991; 91DE-4122160.  
PR 14-DEC-1991; 91DE-4141304.  
PR 21-MAR-1992; 92DE-4209215.  
XX  
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX  
PI Bayer H, Ehrlich-Weinreich G, Ihlenfeldt H, Jung G;  
PI Seidel C, Wienhues U;  
XX  
DR WPI; 1993-009979/02.  
XX  
PT New short hepatitis C virus antigen sequences and corresp.  
PT antibodies - useful in diagnosis and as vaccines  
XX  
PS Claim 1; Page 21 + 14; 22pp; German.  
XX  
CC The sequences of AAR30980-82 are from the C100-3 region of HCV, the  
CC others (AAR30983-92 and AAR33067) from the env/core region. The claimed  
CC sequences are more sensitive than known peptide antigens (e.g. AAR30988)  
CC and, since they are small, can provide a high conc. of reactive sites  
CC with reduced non-specific binding.  
XX  
SQ Sequence 19 AA;  
  
Query Match 45.5%; Score 10; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 12 AVQTNQKLE 21  
Db 1 avqtnwqkle 10  
  
RESULT 4  
AAB28959 standard; peptide; 17 AA.  
XX  
AC AAB28959;  
XX  
DT 29-JAN-2001 (first entry)  
XX  
DE TRFP chain 1 sequence Fel 1.  
XX  
KW Cat; allergy; human T cell reactive feline protein; hTRFP;  
KW immunotherapy.  
XX

OS Felis sp.  
 XX US6120769-A.  
 PN  
 XX 19-SEP-2000.  
 PD  
 XX 28-APR-1995; 95US-0431184.  
 PF  
 XX 02-SEP-1994; 94US-0300928.  
 PR 03-NOV-1989; 89US-0431565.  
 PR 28-FEB-1991; 91US-0662276.  
 PR 13-DEC-1991; 91US-0807529.  
 PR 25-MAR-1992; 92US-0857311.  
 PR 15-MAY-1992; 92US-0884718.  
 PR 15-JAN-1993; 93US-0006116.  
 XX  
 PA (TMU-) IMMULOGIC PHARM CORP.  
 PI Geffer ML, Garman RD, Greenstein JL, Bond JF;  
 PI WPI; 2000-601477/57.  
 DR  
 XX  
 XX  
 PT Detecting, preventing and treating sensitivity to cat protein allergen  
 PT comprises combining a biological sample with a human T cell reactive  
 PT feline protein and determining the extent of binding that occurs -  
 XX  
 PS Example 3; Column 34; 106pp; English.  
 XX  
 CC The present invention relates to the detection of sensitivity to a cat  
 CC protein allergen by combining a blood sample from a subject with a  
 CC peptide of human T cell reactive feline protein (hTRFP). This method  
 CC and the hTRFP peptides are useful for diagnosing, preventing and  
 CC treating cat allergies by reducing or abolishing an individual's  
 CC allergic response to a cat allergen. DNA encoding the TRFP may be  
 CC used as probes to locate equivalent sequences present in other species.  
 CC These may further be used to study the mechanism of immunotherapy of  
 CC cat allergy, and to design modified derivatives, analogues or  
 CC functional equivalents useful in immunotherapy. The present  
 CC sequence was used in the invention.  
 CC  
 SQ Sequence 17 AA;  
 SO

Query Match 22.7%; Score 5; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 ITPAV 13  
 |||||  
 Db 2 itpav 6

RESULT 5  
 ID AAY87702 standard; Protein; 17 AA.  
 XX AAY87702;  
 AC  
 XX 22-AUG-2000 (first entry)  
 DT  
 XX Feline human TRFP peptide Fel 1.  
 DE  
 XX T-cell reactive feline protein: TRFP; Fel d I; cat allergen;  
 KM antiallergic; T cell stimulator; diagnostic; immunotherapy.  
 XX  
 OS Felis sp.  
 XX US6048962-A.  
 PN  
 XX 11-APR-2000.  
 PD  
 XX 27-APR-1995; 95US-0430014.  
 PF  
 XX

PR 02-SEP-1994; 94US-0300928.  
 PR 03-NOV-1989; 89US-0431565.  
 PR 28-FEB-1991; 91US-0662276.  
 PR 13-DEC-1991; 91US-0807529.  
 PR 25-MAR-1992; 92US-0857311.  
 PR 15-MAY-1992; 92US-0884718.  
 PR 15-JAN-1993; 93US-0006116.  
 XX  
 PA (TMU-) IMMULOGIC PHARM CORP.  
 PI Kuo M, Rogers BL, Geffer ML, Morgenstern JP, Brauer AW;  
 PI Greenstein JL, Griffith IJ, Garman RD;  
 PI WPI; 2000-316905/27.  
 DR  
 XX  
 XX  
 PT New human T cell reactive feline protein useful for reducing or  
 PT abolishing individual's allergic response to cat allergen comprising  
 PT two different covalently linked peptide chains -  
 XX  
 PS Example 4; Column 101-102; 106pp; English.  
 XX  
 CC This invention describes a novel naturally occurring cat protein allergen  
 CC (1), human T cell reactive feline protein (TRFP), comprising two  
 CC different covalently linked peptide chains with a molecular weight of 20  
 CC kD, 40 kD or 130 kD under non-reducing conditions and 5 kD or 10-18 kD  
 CC under reducing conditions. The products of the invention have  
 CC antiallergic activity and act as human T cell stimulators. TRFP is useful  
 CC for reducing or preventing the adverse effects of cat allergens on cat  
 CC allergic individuals and in ex vivo diagnostic tests to determine which  
 CC peptides cause sensitivity so as to selectively use them to desensitize  
 CC a cat sensitive individual. Purified TRFP is also useful for studying  
 CC the mechanism of immunotherapy of cat allergy and to design modified  
 CC derivatives, analogs or functional equivalents that are more useful in  
 CC immunotherapy against cat allergy. DNA sequences encoding TRFP are  
 CC useful as probes to locate equivalent sequences present in other species  
 CC (goats, sheep, dogs, rabbits or horses) that may be useful in diagnostics  
 CC and/or therapeutics. Fully defined and characterized TRFP provides  
 CC complete and a very simple desensitization therapy. This sequence  
 CC represents a human T cell reactive feline protein (also known as Fel d 1)  
 CC derived peptide Fel 1 which is described in the method of the invention.  
 CC  
 SQ Sequence 17 AA;  
 SO

Query Match 22.7%; Score 5; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 ITPAV 13  
 |||||  
 Db 2 itpav 6

RESULT 6  
 ID AAY90114 standard; Peptide; 17 AA.  
 XX AAY90114;  
 AC  
 XX 13-JUL-2000 (first entry)  
 DT  
 XX Cat TRFP chain 1 derived peptide, peptide Fel 1.  
 DE  
 XX Cat; TRFP; human T-cell reactive feline protein; cat protein allergen;  
 KM house dust; Fel d I; cat allergy; Felis domesticus sensitivity; therapy;  
 KW diagnosis; goat; sheep; horse; rabbit; dog.  
 XX  
 OS Felis domesticus.  
 XX US6025162-A.  
 PN  
 XX 15-FEB-2000.  
 PD  
 XX

PF 28-APR-1995; 95US-0430944.  
XX  
PR 02-SEP-1994; 94US-0300928.  
PR 03-NOV-1989; 89US-0431565.  
PR 28-FEB-1991; 91US-0662276.  
PR 13-DEC-1991; 91US-0807529.  
PR 25-MAR-1992; 92US-0857311.  
PR 15-MAY-1992; 92US-0884718.  
PR 15-JAN-1993; 93US-0006116.  
XX  
PA (IMMU-) IMMUNOLOGIC PHARM CORP.  
XX  
PI Morgenstern JP, Griffith IJ, Rogers BL;  
XX WPI; 2000-181812/16.  
XX  
DR  
XX  
XX  
PT New human T cell reactive feline protein, useful for desensitizing cat  
PT allergic individuals to cat allergens -  
XX  
XX  
PS Example 4; Column 35; 108bp; English.  
XX  
CC This sequence is a peptide derived from the human T cell reactive feline  
CC protein (TRFP) of the invention. The protein is a cat protein allergen,  
CC and was isolated from a vacuum bag extract obtained by affinity  
CC purification of house dust collected from several homes with cats. TRFP  
CC is composed of two covalently linked peptide chains, and is also referred  
CC to as Fel d I. TRFP and its peptides are useful for reducing or  
CC preventing the adverse effects that exposure to cat allergens normally  
CC has on cat allergic individuals (i.e. to desensitize individuals to cat  
CC allergens or block the effect of the allergens). TRFP is also used in  
CC methods of diagnosing sensitivity to Felis domesticus in an individual.  
CC DNA sequences encoding TRFP can be used as probes to locate equivalent  
CC sequences present in other species, e.g. goat, sheep, horse, rabbit and  
CC dog, that may be useful in diagnostic and/or therapeutic applications.  
XX  
SQ Sequence 17 AA:

Query Match 22.7%; Score 5; DB 21; Length 17;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ITPAV 13  
|||||  
Db 2 itpav 6

## RESULT 7

AAV51499  
ID AAV51499 standard; Protein: 17 AA.

AC AAV51499;

DT 22-MAY-2000 (first entry)

DE Human TRFP derived peptide Fel 1.

XX T-cell reactive feline protein; TRFP: T cell epitope; T cell receptor;  
KW down regulation; immune response; allergen; immunoglobulin E;  
XX sensitivity; cat protein allergen; human.  
OS Homo sapiens.

PN US6019972-A.

PD 01-FEB-2000.

PF 02-SEP-1994; 94US-0300928.

PR 03-NOV-1989; 89US-0431565.

PR 28-FEB-1991; 91US-0662276.

PR 13-DEC-1991; 91US-0807529.

PR 25-MAR-1992; 92US-0857311.

PR 15-MAY-1992; 92US-0884718.  
PR 15-JAN-1993; 93US-0006116.  
XX  
XX  
PA (IMMU-) IMMUNOLOGIC PHARM CORP.  
XX  
PI Garman RD, Greenstein JL, Kuo M, Briner TJ, Morville M, Gelfer ML;  
XX WPI; 2000-146862/13.  
XX  
DR  
XX  
XX  
PT Peptides of human T cell reactive feline protein for treating  
PT sensitivity to cat protein allergens comprise at least one T cell  
PT epitope recognized by a T cell receptor specific for the human T cell  
PT reactive feline protein -  
XX  
XX  
PS Example 4; Column 103-104; 105bp; English.  
XX  
CC This invention describes a novel peptide (I) of human T cell reactive  
CC feline protein (hTRFP) having at least one T cell epitope recognized  
CC by a T cell receptor specific for the human T cell reactive feline  
CC protein, the peptide consisting of at least 7-30 amino acids, and having  
CC an amino acid sequence derived from an amino acid sequence comprising 94,  
CC 96, 97, 109, or 111 residues, given in the specification. The peptides  
CC down regulate the immune response to the allergen. The peptides have  
CC reduced immunoglobulin E binding and reduce T cell responsiveness. The  
CC peptide (I) is useful in compositions for treating sensitivity to a cat  
CC protein allergen in a subject. This sequence represents the human TRFP  
CC derived peptide used in the method of the invention.  
XX  
SQ Sequence 17 AA:

Query Match 22.7%; Score 5; DB 21; Length 17;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ITPAV 13  
|||||  
Db 2 itpav 6

## RESULT 8

AAW61105  
ID AAW61105 standard; peptide: 18 AA.

AC AAW61105;

DT 13-OCT-1998 (first entry)

DE Synthetic alkyl peptide amide inhibitor region.

XX inhibitor region; alkyl peptide amide; peptide moiety; delivery system;  
KW protein kinase; binding; contraceptive; sperm; Hela.

OS Synthetic.

PN WO9822122-A1.

PD 28-MAY-1998.

PF 20-NOV-1997; 97WO-0521509.

PR 21-NOV-1996; 96US-0031428.

PA (PROM-) PROMEGA CORP.

PI Gouell SA;

DR WPI; 1998-332902/29.

PT Alkyl peptide/inhibitor amide compounds - may be used to inhibit

PT binding of one protein to another protein, e.g., to reduce sperm

PT motility

PS Claim 6; Page 48; 66pp; English.  
XX  
CC The sequence is that of the inhibitor region of an alkyl peptide amide.  
CC The region comprises a sequence of amino acids homologous to a binding  
CC domain of a first protein. The binding domain is capable of binding a  
CC second protein in the intracellular space of a living cell. Such a  
CC peptide may be used to inhibit binding of the first protein to the  
CC second protein especially when the second protein is protein kinase  
CC A and the first protein is a protein kinase binding domain of an  
CC anchor region. Such peptides are efficient delivery systems for  
CC introducing peptide moieties into the intracellular space of  
CC living cells, including sperm cells and HeLa cells. The motility  
CC of sperm cells can be inhibited after exposure to the alkyl peptide  
CC amide form of anchor inhibitor peptides. These amides can thus be  
CC used, e.g., as contraceptives.  
XX  
SQ Sequence 18 AA;

Query Match 22.7%; Score 5; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 AEVIT 10  
| | | | |  
Db 8 aeait 12

RESULT 9  
AAV56950  
ID AAV56950 standard; peptide; 18 AA.  
XX  
AC AAV56950;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE PKA RII subunit binding peptide AKAP 95 (residues 642-659).  
XX  
XX Fatty acid; amphipathic; RII subunit; protein kinase A; PKA;  
KM sperm A kinase; anchoring protein; contraception; sperm motility.  
XX  
OS Synthetic.

XX US6011013-A.  
XX  
XX 04-JAN-2000.  
XX  
XX 18-JUN-1998; 9805-0100789.  
XX  
XX 20-JUN-1997; 9705-0050314.  
XX  
XX (UYOR-) UNIV OREGON HEALTH SCI.  
XX  
XX Vijayaraghavan S, Carr DW;  
XX  
XX WPI; 2000-136197/12.  
XX

PT Contraceptive composition containing fatty acid conjugate of peptide  
PT that inhibits protein kinase A binding to sperm A kinase anchoring  
PT proteins  
XX  
XX Claim 3; Column 5; 12pp; English.  
XX

XX The invention provides a contraceptive composition that comprises a  
CC conjugate of a synthetic peptide and a fatty acid, where the peptide  
CC comprises an amphipathic alpha-helix domain that binds to an RII subunit  
CC of protein kinase A (PKA) and competitively inhibits binding of PKA to  
CC sperm A kinase anchoring proteins. The composition and method are useful  
CC for contraception by inhibiting sperm motility. Sequences AAV56946-956  
CC represent synthetic peptides that bind to the RII subunit of PKA.  
XX  
XX Sequence 18 AA;

Query Match 22.7%; Score 5; DB 21; Length 18;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 AEVIT 10  
| | | | |  
Db 8 aeait 12

RESULT 10  
AAW05816  
ID AAW05816 standard; peptide; 6 AA.  
XX  
AC AAW05816;  
XX  
DT 09-JUL-1997 (first entry)  
XX  
DE TNFalpha residues 29-34 antisense peptide afnTIII.  
XX

XX Antisense peptide; hydropathic peptide; antagonist; interleukin-1beta;  
KM IL-1beta; cytokine; cancer; inflammatory condition; rheumatoid arthritis;  
KM septic shock; therapy; IL-1alpha; IL-8; tumour necrosis factor alpha;  
XX TNFalpha; ectoxin.  
XX  
OS Synthetic.

XX W09634887-A2.  
XX  
XX 07-NOV-1996.  
XX  
XX 07-MAY-1996; 9600-GH01082.  
XX  
XX 11-APR-1996; 96GB-0007505.  
XX  
XX 05-MAY-1995; 95GB-0009263.  
XX  
XX (UNLO ) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.  
PA (UNLO ) LONDON SCHOOL HYGIENE & TROPICAL MEDICIN.  
XX  
XX Miller AD, Raynes JG;  
PI  
XX  
XX WPI; 1996-506102/50.  
XX

XX Antisense peptide(s) which alter the activities of target  
PT cytokine(s) - used to treat inflammatory conditions e.g. Rheumatoid  
PT arthritis or cancer  
XX  
XX Claim 10; Page 29; 41pp; English.

XX AAW05812-W05819 represent antisense peptides of the invention. Antisense  
CC peptides are encoded by antisense DNA. The antisense peptides are the  
CC hydropathic complement of the peptides encoded by the sense DNA strand.  
CC Antisense peptides exert an antagonistic effect on target ligands by  
CC virtue of their ability to bind to the sense peptide sequences, and  
CC thereby competing with the normal binding ligands for the peptide. These  
CC sequences are antisense to a target polypeptide, and when bound to their  
CC targets, alter the biological activity of the target polypeptide or the  
CC activity of a target molecule containing the peptide. AAW05814-W05816  
CC are antisense to a sequence contained within tumour necrosis factor  
CC alpha (TNFalpha). These sequences are used to treat or prevent  
CC conditions mediated by cytokines, preferably cancer or inflammatory  
CC conditions, especially rheumatoid arthritis or septic shock.  
XX  
XX Sequence 6 AA;

Query Match 18.2%; Score 4; DB 17; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 11 PAVQ 14  
| | | | |  
Db 3 pavq 6

```
RESULT 11
AAW6749
XX AAW6749 standard; Protein: 6 AA.
AC AAW6749;
XX
XX 15-JAN-1999 (first entry)
XX
XX Murine signalling chimeric protein peptide #14.
XX
XX Induction: intracellular aggregation; cytoplasmic tail; zeta chain;
XX T cell receptor/CD3 complex; signal; transcription; reporter gene;
XX homodimerization; Fas receptor; cell-specific apoptosis; Gal4; VP16;
XX heterodimerization; primer.
XX
XX Mus sp.
XX
XX US5830462-A.
XX
XX 03-NOV-1998.
XX
XX 07-JUN-1995; 95US-0478386.
XX
XX 14-FEB-1995; 95US-0388653.
XX
XX 12-FEB-1993; 93US-0017931.
XX
XX 16-JUL-1993; 93US-0092977.
XX
XX 07-JAN-1994; 94US-0179748.
XX
XX 11-FEB-1994; 94US-0196043.
XX
XX 18-AUG-1994; 94US-0292597.
XX
XX 07-JUN-1995; 95US-0478386.
XX
XX (HARD ) HARVARD COLLEGE.
XX (STRD ) UNIV LELAND S STANFORD.
XX
XX Belshaw P, Crabtree GR, Schreiber SL, Spencer DM;
XX Wandless TJ;
XX
XX WPI; 1998-609192/51.
XX N-PSDB; AAV62963.
XX
XX Inducing a biological process in a cell using ligand-induced gene
XX expression for e.g. cell death - using DNA construct encoding
XX ligand-binding domain and dimerisable protein domain
XX
XX Example 5; Column 81-82; 95pp; English.
XX
XX AAW6736-W6764 are peptides used to design primers used in a novel
XX method for inducing a biological process in a cell. The method can be
XX used to induce the intracellular aggregation of the cytoplasmic tail of
XX the zeta chain of the T cell receptor/CD3 complex, leading to signalling
XX and transcription of a reporter gene. The method also has applications
XX for the homodimerization of the cytoplasmic tail of the Fas receptor.
XX leading to cell-specific apoptosis and for the heterodimerization of Gal4
XX and VP16, leading to direct transcription of a reporter gene.
XX
XX Sequence 6 AA:
SQ
Query Match 18.2%; Score 4; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 19 KLEV 22
| | | |
DB 3 Klev 6
RESULT 12
AAW92484
XX AAW92484 standard; Protein: 6 AA.
XX
```

```
AC AAW92484;
XX
XX 21-APR-1999 (first entry)
XX
XX Murine signalling chimeric protein for primer 6053.
XX
XX Inducible; regulated; dimerisation; oligomerisation; control mechanism;
XX intracellular protein; activation; aggregation; cytoplasmic tail; Gal4;
XX zeta chain; T cell receptor; TCR-CD3 complex; reporter gene; VP16;
XX Fas receptor; cell specific apoptosis; DNA binding domain; chimeric;
XX transcription-activation domain; murine; chimeric protein.
XX
XX Mus sp.
XX
XX US5869337-A.
XX
XX 09-FEB-1999.
XX
XX 14-FEB-1995; 95US-0388653.
XX
XX 14-FEB-1995; 95US-0388653.
XX
XX 12-FEB-1993; 93US-0017931.
XX
XX 16-JUL-1993; 93US-0092977.
XX
XX 07-JAN-1994; 94US-0093499.
XX
XX 07-JAN-1994; 94US-0179148.
XX
XX 11-FEB-1994; 94US-0196043.
XX
XX 18-AUG-1994; 94US-0292597.
XX
XX (HARD ) HARVARD COLLEGE.
XX (STRD ) UNIV LELAND S STANFORD.
XX
XX Belshaw P, Crabtree GR, Schreiber SL, Spencer DM;
XX Wandless TJ;
XX
XX WPI; 1999-152789/13.
XX N-PSDB; AAX02047.
XX
XX Genetic constructs encoding chimeric protein - comprise
XX ligand-binding domain and action domain
XX
XX Example 5; Fig 4C; 96pp; English.
XX
XX This invention describes a novel method for the regulated (inducible)
XX dimerisation or oligomerisation of intracellular proteins. Dimerisation
XX and oligomerisation of proteins are general biological control
XX mechanisms that contribute to the activation of cell membrane receptors,
XX transcription factors, vesicle fusion proteins and other classes of
XX intra- and extra-cellular proteins. The invention describes a method for
XX inducing the intracellular aggregation of the cytoplasmic tail of the
XX zeta chain of the T cell receptor (TCR)-CD3 complex leading to
XX signalling and transcription of a reporter gene, the homodimerisation of
XX the cytoplasmic tail of the Fas receptor leading to cell specific
XX apoptosis and the heterodimerisation of a DNA binding domain (Gal4) and
XX a transcription-activation domain (VP16) thereby leading to direct
XX transcription of a reporter gene. AAW92471-W92485 are murine signalling
XX chimeric protein fragments used to design the primers represented in
XX AAX02029-X02049.
XX
XX Sequence 6 AA:
SQ
Query Match 18.2%; Score 4; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 19 KLEV 22
| | | |
DB 3 Klev 6
RESULT 13
AAB03568
```

ID AAB03568 standard; Peptide: 6 AA.  
XX AAB03568;  
AC  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Murine signalling chimeric protein construction peptide SEQ ID NO:36.  
XX  
KM dimerisation; oligomerisation; biological control mechanism;  
KM chimeric; expression regulation; gene therapy; cardiant; vasotropic;  
KM cerebroprotective; analgesic; immunosuppressive; cytostatic;  
KM osteopathic; stroke; reperfusion injury; autoimmune disease;  
XX chronic pain; osteoporosis; cancer.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
PN US6063625-A.  
PD 16-MAY-2000.  
XX  
XX 16-SEP-1998; 9805-0156655.  
XX  
PR 14-FEB-1994; 9405-0196043.  
PR 12-FEB-1993; 9305-0017931.  
PR 16-JUL-1993; 9305-0092977.  
PR 16-JUL-1993; 9305-0093499.  
PR 07-JAN-1994; 9405-0179143.  
PR 07-JAN-1994; 9405-0179748.  
XX  
PA (STRD ) UNIV LELAND S STANFORD.  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Schreiber SL, Spencer DM, Wandless TJ, Belshaw P, Ho SN;  
PI Crabtree GR;  
XX  
DR WPI; 2000-375496/32.  
XX  
PT Regulating expression of targeted genes in cells; useful for regulated  
PT gene therapy; comprises treating cells with membrane permeable  
PT synthetic ligand which binds to the receptor domain to dimerize or  
PT oligomerize the proteins -  
PS  
XX Example 5; Fig 4; 92pp; English.  
XX  
CC The present invention describes a method for regulating expression of a  
CC target gene. The method comprises providing a muscle or liver cell  
CC containing nucleic acids (N1 and N2) encoding chimeric proteins (P1 and  
CC P2) with ligand-binding and transcriptional activation domains and  
CC exposing the cells to a ligand. The method is useful in the basic  
CC investigation of a variety of cellular processes and in regulating the  
CC synthesis of proteins of therapeutic or agricultural importance. The  
CC method is useful in exocytosis, where export of a protein rather than  
CC transcription is controlled by the ligand, as well as in the control of  
CC protein degradation or activation. The method and the modified cells are  
CC especially useful in gene therapy, e.g., in the treatment of cardiac  
CC patients or patients susceptible to stroke, reperfusion injury,  
CC autoimmune disease, chronic pain, osteoporosis, or gene therapies  
CC involving cells which may have to be destroyed (e.g., cancerous cells or  
CC modified cells that result in another pathogenic state), as well as in  
CC other applications where inducible transcription or translation is  
CC desired. The cells can also be used in vivo, to modify whole organisms,  
CC preferably animals, including humans. The method permits regulated gene  
CC therapy, therefore increasing the safety, expression level and overall  
CC efficacy. AAA60476 to AAA60521 and AAB03554 to AAB03581 represent  
CC sequences used in the exemplification of the present invention.  
XX  
XX Sequence 6 AA:

Query Match 18.2%; Score 4; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 KLEV 22  
DB 3 KLEV 6  
RESULT 14  
ID AAY90488 standard; peptide: 6 AA.  
XX AAY90488;  
AC  
XX  
DT 15-AUG-2000 (first entry)  
XX  
DE Peptide encoded by complement of PCR primer P#6052, SEQ ID NO:36.  
XX  
XX Fusion protein; ligand-binding domain; action domain;  
KM ligand-induced dimerisation; oligomerisation; intracellular signalling;  
KM apoptosis; transcriptional activation; cancer; infectious disease;  
KM metabolic deficiency; cardiovascular disease; autoimmune disease;  
XX endocrine abnormality; gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX  
PN US6046047-A.  
PD 04-APR-2000.  
XX  
XX 16-SEP-1998; 9805-0157230.  
XX  
PR 14-FEB-1995; 9505-0388653.  
PR 12-FEB-1993; 9305-0017931.  
PR 16-JUL-1993; 9305-0092977.  
PR 16-JUL-1993; 9305-0093499.  
PR 07-JAN-1994; 9405-0179143.  
PR 07-JAN-1994; 9405-0179748.  
PR 14-FEB-1994; 9405-0196043.  
PR 18-AUG-1994; 9405-0292597.  
XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Schreiber SL, Spencer DM, Crabtree GR, Belshaw P, Ho SN;  
PI Wandless TJ;  
XX  
XX WPI; 2000-282689/24.  
XX  
DR New chimeric proteins comprising a ligand binding domain and an  
PT intracellular targeting domain, and genetic constructs encoding the  
PT chimeric proteins, useful for regulated production of desired proteins,  
PT as well as for gene therapy -  
XX  
XX Disclosure; Fig 4C; 94pp; English.  
XX  
CC The invention relates to chimeric proteins and small organic molecules  
CC capable of binding to two or more chimeric protein molecules, thereby  
CC oligomerising them. The chimeric proteins comprise one or more ligand-  
CC binding domains fused to one or more "action" domains which are  
CC heterologous with respect to the ligand binding domain. The ligand-  
CC binding domain may, for example, be an FKBP protein, capable of binding  
CC FK506-type ligands. Examples of action domains include Fas (which, when  
CC cross-linked, triggers apoptosis); domains involved in intracellular  
CC signalling such as the CD3 zeta subunit or the Interleukin-2 receptor  
CC (Tac); DNA binding proteins such as GAL4 or HNF1; or a transcriptional  
CC activator such as VP16. The chimeric protein may contain additional  
CC domains such as intracellular targeting domains. Examples of the  
CC chimeric proteins constructed include an immunophilin-Fas chimeric  
CC protein; a chimeric murine signalling protein comprising an  
CC Interleukin-2 receptor moiety (Tac), the transmembrane and cytoplasmic  
CC domains of CD3 and human FKBP12; and a GAL4 DNA binding domain/FKBP  
CC domain/epitope tag fusion protein. The chimeric proteins, genetic  
CC constructs encoding the chimeric protein and vectors are useful for the  
CC treatment of many conditions, e.g., cancer, infectious diseases,

CC metabolic deficiencies, cardiovascular diseases, autoimmune diseases or  
CC endocrine abnormalities. The chimeric proteins encoded by the genetic  
CC constructs are useful for regulated production of a desired protein, and  
CC in gene therapy. They are also useful in conjunction with the expression  
CC of an exogenous protein, properly encoded for transport to a vesicle, or  
CC for an endocytotic endogenous protein to enhance export of the endogenous  
CC protein. The oligomerisation mechanism is useful for control of protein  
CC degradation or inactivation. Homologous recombination is useful to remove  
CC or inactivate endogenous transcriptional control sequences. Sequences  
CC AA190474-190501 represent peptides encoded by oligonucleotides which were  
CC used in the exemplifications and disclosure of the invention in the  
CC construction of genetic constructs encoding the chimeric proteins of the  
CC invention.

Query Match	18.2%	Score 4:	DB 21:	Length 6:
Best Local Similarity	100.0%	Pred. No. 3.4e+05:		
Matches	4:	Conservative	0:	Mismatches 0:
				Indels 0:
				Gaps 0:
QY	19	KLEV	22	
Db	3	klev	6	

**RESULT 15**

ID AAB60832 standard; peptide; 6 AA.

AC AAB60832;

DT 29-MAR-2001 (first entry)

DE Peptide #14 encoded by primer of the invention.

KW protein expression; gene therapy; cancer; infection;  
KW cardiovascular; metabolic; coagulation; autoimmune; arthritis  
KW pulmonary; kidney; endocrine.

OS Unidentified.

PN US6165787-A.

PD 26-DEC-2000.

PF 29-MAY-1998; 98US-0087647.

PR 14-FEB-1995; 95US-0388653.

PR 12-FEB-1993; 93US-0017931.

PR 16-JUL-1993; 93US-0093499.

PR 07-JAN-1994; 94US-0179748.

PR 14-FEB-1994; 94WO-US01617.

XX

PA (HARD ) HARVARD COLLEGE.

PI Schreiber SL, Crabtree GR, Wandless TJ, Belshaw P, Spencer DM;

DR WPI; 2001-079849/09.

PT Novel eukaryotic cell useful in gene therapy for treating cancer,  
PT infectious and autoimmune diseases, comprises genetic construct  
PT encoding chimeric protein which comprises ligand-binding and action  
PT domains -

PS Examples; Fig 4; 97pp; English.

CC The present invention relates to a eukaryotic cell, comprising  
CC vector encoding a chimeric protein which has a  
CC ligand-binding domain which forms ligand cross-linked protein  
CC complexes including the chimeric protein, and a heterologous  
CC action domain. The invention is useful in gene therapy for  
CC treating cancer, infectious diseases, metabolic deficiencies,  
CC cardiovascular diseases, hereditary coagulation deficiencies,  
CC autoimmune diseases, joint degenerative diseases e.g.  
CC arthritis, pulmonary disease, kidney disease, and endocrine  
CC abnormalities.  
XX  
CC  
Sequence 6 AA:  
50

Query Match	18.2%	Score 4	DB 22	Length 6
Best Local Similarity	100.0%	Pred. No.	3.4e+05	
Matches 4	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	19	KLEV	22
Db	3	klev	6

```
Search completed: July 23, 2001, 16:56:11
Job time: 528 sec
```

~ Immunologically  
Equivalent?

from binder?

Marver duPont